

Group 5

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 523 bits (1346), Expect = 6e-146
 Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

Query	371	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEEL	430
	P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L		
Sbjct	4	PNVVTTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNITYGTIVDGMCKMGDTVSALNL	63
Query	431	YDEMLPRGII-PNTIYTSSMIDGFCKQNRLDAEHHMFYLMATKGCPNLITFNTLIDGYC	489
	+M I P+ +YS-+IDG K R A++F M KG P++T++ +I+G+C		
Sbjct	64	LRKMEELSHIKPDPVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPPDIVTYSCMINGFC	123
Query	490	GAKRIDDGSELLHEMETETGLVADTTTNYTLIHGFYLVVGDLNAALDLLQEMISSGLCPDIV	549
	+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V		
Sbjct	124	SSGKWEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNV	183
Query	550	TCDTLLDGLCDNGKLKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGK	609
	TC+TLLDGLCD GKLDALEMFK MQKS D+DA-H FNGVEPDVQTYNILISGLINEGK		
Sbjct	184	TCNTLLDGLCDRGKLKDALEMFKAMQSKSMMIDATAHAFNGVEPDVQTYNILISGLINEGK	243
Query	610	FLEAAELYEEMPHRGIIVPDTITYSSMIDGLCKQSRLDEATQMFDMSGSKSFSPNVVTFTT	669
	FLEAAELYEEMPHRGIIVPDT-TYSSMI-GLCKQSRLDEATQMFDMSGSKSFSPN+VTF T		
Sbjct	244	FLEAAELYEEMPHRGIIVPDTVYTSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTFNT	303
Query	670	LINGYCKAGRVDGELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSG	729
	LI GYCKAG VDDGLELFCEMGRRGIVANAITYITLIC GFRKVGNING+LDIFQEMISSG		
Sbjct	304	LITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSG	363
Query	730	VYPDTITIRNMLTGLWSKEELKRAVAMLELKQMSMVYI	767
	VYPDTITIRNMLTGLWSKEELKRA-AMLE+LQMSMV +		
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRALAMLELQMSMVSF	401

Score = 394 bits (1012), Expect = 3e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	263	CRPNVVTFTTLMNGLCREGRIVEAVALLDRMVEDGLQPQTITYGTIVDGMCKKGDTVSAL	322
	C+PNVVFTFTLMNGLCREGR+VEAVALLDRM+EDGLQP QITYGTIVDGMCK GDTVSAL		
Sbjct	2	CKPNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNITYGTIVDGMCKMGDTVSAL	61
Query	323	NLLRKMEEVSHIIPNWWIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPPDLFTYNSMIVG	382
	NLLRKMEE+SHI P++VIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G		
Sbjct	62	NLLRKMEELSHIKPDPVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPPDIVTYSCMING	121
Query	383	FCSSGRWSDAEQLLQEMLERKISPDPVVTYNALINAFVKEGKFFAEELYDEMLPREGIIPN	442
	FCSSG+WS+A++LLQEML RKISPDPVVT++ LINA VKEG A++L EM+ G+ PN		
Sbjct	122	FCSSGKWEAQRLLQEMLVRKISPDPVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN	181

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Query	443	TITYSSMIDGFCKQNRLDAEHMFYLM-----	ATKGCPNLITFNTLIDGYCGA	491
		+T +++DG C + L A MF M	A G P+ T+N LI G	
Sbjct	182	VVTCNTLLDGLCDRGKLDKALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLINE		241
Query	492	KRIDDGSELLHEMTETGLVADTTTYNTLIHGFLVGDLNAAQLLQEMISSGLCPDIVTC		551
		+ + EL EM G+V DT TY++I+G L+ A + M S P+IVT		
Sbjct	242	GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSNIVTF		301
Query	552	DTLLDGLCDNGKLKDALEMFKVMQSKKDLDAHFPNFGVEPDVQTYNILISGLINEKGFL		611
		+TL+ G C G + D LE+F M + G+ + TY LI G G		
Sbjct	302	NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYITLIRGFRKVGNIN		350
Query	612	EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSM		655
		+ +++EM G+ PDTIT +M+ GL + L A M + +		
Sbjct	351	GSLDIFQEMISSGGVYPDTITIRNMLTGLWSKEELKRALAMLEEL		394

Score = 300 bits (767), Expect = 8e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query	230	PDVVFTTLLHGLCVEDRVSEALDFHQMFFETTCCRPNVFTTLMNGLCREGRIVEAVAL		289
		P+VVTFTT+GLC E RV EA+ +M E -PN +T+ T++G+C+ G V A+ L		
Sbjct	4	PNVNTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCRMGDTVSALNL		63
Query	290	LDRMBE-DGLQPTQITYGTIVDGMCKGDTVSALNLLRMEEVSHIIPNVIYSAIIDS		348
		L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+		
Sbjct	64	LRKMEELSHIKPDVVIIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF		122
Query	349	CKDKGRHSQDAQNLFTEMQEKGJFPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----		401
		C G+ S-AQ L EM + I PD+ T++ +I G + A+ LLQEM+		
Sbjct	123	CSSGKWSEAQRLLQEMILVRKISPDVVTFSGLINALVKEGDLNQAQDLLQEMISSGVCPNV		182
Query	402	-----RKiSPDVVTYNALINAFVKEG		422
		+ PDV TYN LI+ + EG		
Sbjct	183	VTCNTLLDGLCDRGKLDKALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLINEG		242
Query	423	KFEEAEELYDEMFLPRGIIPN7ITYSSMIDGFCKQNRLDAEHMFYLMATKGCSPNLITFN		482
		KF EAEELY-EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN		
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSNIVTF		302
Query	483	TLIDGYCKAKRIDDGSELLHEMTETGLVADTTTYNTLIHGFLVGDLNAAQLLQEMISS		542
		TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS		
Sbjct	303	TLITGYCKAGMVDDGLELFCEMGRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS		362
Query	543	GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS	577	
		G+ PD +T +L GL +LK AL M + +Q S		
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS		397

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Score = 216 bits (551), Expect = 8e-54
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query 160	PSVVDCKLGMGVVRMERPDVLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST P+VV F LM + R R ++L +M ++ + ++ ++ C AL+	219
Sbjct 4	PNVTTTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSALNL	63
Query 220	FGKITKLG-LHPDVVTTTLLHGLCVEDRVSEALDFFIQMFETTCRPNVVTFTLMNGLC K+ +L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	278
Sbjct 64	LRKMEELSHIKPDVVVIYSAIDIGLWKDGRHTDAQNLFIEMQDKGIFIPDIVTYSCMINGFC	123
Query 279	REGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV G+ EA LL M+ + P +T+ +++ + K+GD SA +LL+ +M S + PNV	338
Sbjct 124	SSGKWSAQRLQEQMLVRKISPDVVTFTSGLINALVKEGDLNSAQDQLQEMIS-SGVCNPV	182
Query 339	VIYSAIDISSLCKDGRHSIDAQNLFTEMQE-----KGIFPDLFYTNSMIVGFCSSG V + ++ D LC G+ DA +F MO+ G+ PD+ TYN +I G + G	387
Sbjct 183	VTCNTLDGLCDRGKLDALEMFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISLINEG	242
Query 388	RWSDABQQLQEMMLERKISPDVVTYNALINAFVKEGKFEEAEELYDEMPLPRGIIPNTITYS ++ +AB+L +EM R I PD VTY+ ++IN K+ + EA + ++D M + PN +T++	447
Sbjct 243	KFLEAAELYEEMPHRGIVPDVTYSSMINGLCKQSRLDEATQMFDSMSGSKSFSPNIVTFN	302
Query 448	SMIDGFCKQNRLDAAEIIMFYLMATKGCSPLNITFTNLTIDGYCGAKRIDGMELLHEMTET ++ +I G+CK +D +F M +G N IT+ TLI G+ I+ + ++ EM +	507
Sbjct 303	TLITGYCKAGMVDDGLELFCEMGRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS	362
Query 508	GLVADTTTYNTLIGHFYLVGLDNAALDLLQEM 539 G+ DT T ++ G+ +L AL +L+E+	
Sbjct 363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394	

Score = 193 bits (491), Expect = 8e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query 145	DAIDLFSMLRSRPLPSVVDCKLGMGVVRMERPDVLVISLYQKMER-KQIRCDIYSFNIL +A+ L M+ P+ + ++ + +M ++L +KME I+ D+ ++ +	203
Sbjct 24	EAVALLDRMRVEDGLQPQNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVVIYSAI	83
Query 204	IKCFCSKSKLPFALSTFGKITKLG-LHPDVVTTTLLHGLCVEDRVSEALDFFIQMFETTC I + A + F ++ G+ PD+VT++ ++ +G C + SEA +M	263
Sbjct 84	IDGLWKDGRHTDAQNLFIEMQDKGIFIPDIVTYSCMINGFCSSGKWSAQRLQEMLVRKI	143
Query 264	RPNVVTPTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN P+VVTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL	323
Sbjct 144	SPDVVTFSGLINALVKEGDLNSAQDQLQEMISSGVCNPVVTCTNLLDGLCDRGKLDALE	203
Query 324	LLRKME-----EVSH----IIIPNVVIYSAIDISSLCKDGRHSIDAQNLFTEMQEKGIFIPDL + + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD	373
Sbjct 204	MFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISLINEGKFLEAAELYEEMPHRGIVPDT	263

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Query	374	FTYNNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVNTYNALINAFVKEGKFEEAEELYDE	433
		TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E	
Sbjct	264	VTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTNTLITGYCKAGMVDDGLELFCE	323
Query	434	MLPRGIIPNNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPNLITFNTLIDGYCGAKR	493
		M RG+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +	
Sbjct	324	MGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSGGVYPDTITIRNMLTGLWSKEE	383
Query	494	IDDGMELLHEM 504	
		+ + + +L E+	
Sbjct	384	LKRALAMLEEL 394	

Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query	135	SGFHEIKGLEDAIDLFSMDLRSRPLPSVVFDFCKLGMGVVRMERPDVLVISLYQKMERKQIR	194
		+GF +A L +ML + P VV F L+ +V+ + L Q+M +	
Sbjct	120	NGFCSSGKWSSEAQRLLQEMLVRKISPVDVTFSGLINALVKEGDLNSAQDLLQEMISSGVC	179
Query	195	CDIYSFNILIKCFCSCSKLPFALSTFGKITKL-----GLHPDVVTFTTLHGLC	243
		++ + N L+ C KL AL F + K G+ PDV T+ L+ GL	
Sbjct	180	PNVVTCTNLLDGLCDRGKLKDALEMFKAMQKSMMDDIDATHAFNGVEPDVQTYNILISGLI	239
Query	244	VEDRVSSEALDFFHQMFTTCRPNVTTFTLMNGLCREGRIVEAVALLDRRMEDGLQPTQI	303
		E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +	
Sbjct	240	NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIV	299
Query	304	TYGTIVDGMCKKGDTDSALNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFT	363
		T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E	
Sbjct	300	TFNTLTGYCKAGMVDDGLELFCEMGRG-IVANAITYITLIRGFRKVGNINGSLDIFQE	358
Query	364	MQEKGIFPDLFYTNSMIVGFCSSGRWSDAEQLLQEMLERKIS 405	
		M G++PD T +M+ G S A +L+E+ +S	
Sbjct	359	MISSGGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

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- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found

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- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1180 bits (3053), Expect = 0.0
Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query 84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct 1	MLARVCRFE SSSSSSVAARFFCTGSIRHALAEKSRDGEAGFRGESLKLRLSGSYEIK	60
Query 142	GLEDAIDLFSMDLRSRPLPSVVFCKLMGVVVVRMERPDLDLVISLYQKMERKQIRCDIYSFN	201
	GLEDAIDLFSMDLRSRPLPSV+DF KLMG VVRMERPDLDLVISLYQKMERKQIRCDIYSF	
Sbjct 61	GLEDAIDLFSMDLRSRPLPSVIDFNKLMGA VVRMERPDLDLVISLYQKMERKQIRCDIYSFT	120
Query 202	ILIKCFCSCKLPFALSTFGKITKGLHLPDVVTFTLLHGLCVEDRVSEALDFFHQMFT	261
	ILIKCFCSCKLPFALSTFGK+TKLGLHPDVVTFTLLHGLC++ RVSEALD FHQ+	
Sbjct 121	ILIKCFCSCKLPFALSTFGKLTKGLHLPDVVTFTLLHGLCLDHRS EVSEALDLFHQI---	177
Query 262	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSA	321
	CRP+V+TFTTLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDGMC K GDTVSA	
Sbjct 178	-CRPDVLTF TLMNGLCREGRVVEAVALLDRMVENGLQPDQITYGTFVDGMCKM GDTVSA	236

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Query	322	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNMSIV	381
Sbjct	237	LNLLRKMEE-SHI PNVVIYSAIID LCKDGRHS+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQEMLERKISPVVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFC SGRWS A+-LLQEMLERKISP+VVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPNLTIFNTLIDGYCGAKRIDDGMELL	501
Sbjct	357	NTITY-SMIDGFCKQ+RLDAA MFYLMATKGCP++ TF TLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLAVADTTTYNTLIIHGFYLVGDLNAAALDLQEMISSGLCPDIVTCDTLLDGLCDN	561
Sbjct	417	HEM GLVA-T TYNTLIIHGF LVGDLNAAALDL Q+MISSG-CPDIVTC+TLLDGLCDN	476
Query	562	GKLKDALEMFKVMQSKKKLDASHPFNGVPDVQTYNILISGLINEGKFLEAEELYEEMP	621
Sbjct	477	GKLKDALEMFKMOKSK DLDASHPFNGVPDV TYNIL GLINEGKFLEAEELYEEMP	536
Query	622	HRGIVPDITYYSSMIDGLCKQSRLDEATQMFDSMGSKSFSFSPNVTFTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDITYYSSMIDGLCKQSRLDEATQMF SMGSKSFSFSPNVTFTTLINGYCKAGRVD	596
Query	682	DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCEMGRRGIVADAIIYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMELKLMQSMVY	766
Sbjct	657	TG WSKEL-RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1624 bits (4206), Expect = 0.0
 Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSHTYSFGFSSLFGFRIFGVKDFSPIRFLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSHTYSFGFSSLFGFRIFGVKDFSPIRFLFLNYGSGSVRI	60
Query	61	LADSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSPAESAARLFCTRSIRDTLAKASGE	120

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Query	121	SCEAGF GGESLKLQSGFHEIKGLEDAIDLFSMLRSRPLPSVVD FCKLMGVVV RMERPD L	180
Sbjct	121	SCEAGF GGESLKLQSGFHEIKGLEDAIDLFSMLRSRPLPSVVD FCKLMGVVV RMERPD L	180
Query	181	VISLYQKMERKQIRC D IYSFNILIKCFCSCSKLPF ALSTFGKITKGLH PDVVFTTLLH	240
Sbjct	181	VISLYQKMERKQIRC D IYSFNILIKCFCSCSKLPF ALSTFGKITKGLH PDVVFTTLLH	240
Query	241	GLCVEDRVSEALDEFHQM FETTCRPN VFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDEFHQM FETTCRPN VFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKG DTVSALNLLRKMEEVSHIIPN VVIYSAIIDS LCKDGRHS DAQNL	360
Sbjct	301	TQITYGTIVDGMCKKG DTVSALNLLRKMEEVSHIIPN VVIYSAIIDS LCKDGRHS DAQNL	360
Query	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLQ EMLERKISPDVVTYNA FVK	420
Sbjct	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLQ EMLERKISPDVVTYNA FVK	420
Query	421	EGKF FEAEEELYDEMLPRGIIP PNTIT YSSMIDGFCKQNRL DAAEHMFYLMATKG CSPN LIT	480
Sbjct	421	EGKF FEAEEELYDEMLPRGIIP PNTIT YSSMIDGFCKQNRL DAAEHMFYLMATKG CSPN LIT	480
Query	481	FNTL IDGYCGAKR IDGMELLHEMTETGLVADTTT NTL IHGFYLVGD LNA ALD L QEMI	540
Sbjct	481	FNTL IDGYCGAKR IDGMELLHEMTETGLVADTTT NTL IHGFYLVGD LNA ALD L QEMI	540
Query	541	SSGLCP DIVCTD LLDGLCDNGKLKALEMFKV MOKSK KLDASHPFNGVEPDVQ TYNIL	600
Sbjct	541	SSGLCP DIVCTD LLDGLCDNGKLKALEMFKV MOKSK KLDASHPFNGVEPDVQ TYNIL	600
Query	601	ISGLINEGKFLEAEELYEEMPHRGIVPPDTITYSSMID GLCKQS RLDEATQ MFDSM GS KSF	660
Sbjct	601	ISGLINEGKFLEAEELYEEMPHRGIVPPDTITYSSMID GLCKQS RLDEATQ MFDSM GS KSF	660
Query	661	SPNVFTTTLINGYCKAGR VDDGLELFCEMGR RGIVANA ITYITLICGFRKVGN INGAL D	720
Sbjct	661	SPNVFTTTLINGYCKAGR VDDGLELFCEMGR RGIVANA ITYITLICGFRKVGN INGAL D	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAM LEKLO QMSMVYYWSELKRHTFQK IS	780
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAM LEKLO QMSMVYYWSELKRHTFQK IS	780
Query	781	GVKRCLGVCPCFCSCHHGYQRARSS	804
Sbjct	781	GVKRCLGVCPCFCSCHHGYQRARSS	804

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)

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Score = 975 bits (2521), Expect = 0.0
 Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query 84	MLARVCGFKCSSSPAESAARLFCTRDIRTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
	MLARV SSSPA SAARLFCTRIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct 1	MLARVYRSGSSSSPAVAESAARLFCTRIRHALAKSRDG-ESGFGGESLKLRSGFHEIKGL	59
Query 144	EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDVLVISLYQKMERKQIRCIDIYSFNIL	203
	EDAIDLF DM+RSPRLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct 60	EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query 204	IKCFCSCSKLPALSTFGKITKLGHLHPDVVTFTLLHGLCVEDRVSEALDDFHQMFTTC	263
	+KCFCSCKLPALSTFGKITKLG	FH
Sbjct 120	MKCFCSCKLPALSTFGKITKLG-----	FH-----
Query 264	RPNVVTFTTLMNGLCREGRIVEAVALLDLRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
	P VVTF+CL+ +GLC E RI AE + L +M + P +T+ T+++G+C++G V A+	
Sbjct 146	-PTVVFTSTLLHGLCVEDRIVESEALDDLFHQMCK---PNVVTFTTLMNGLCREGRVVEAVA	200
Query 324	LLRKMEEVSHIIPNVVIYSAIIDSCLKDGRHSQAQNLTTEMQEKG-I FPDLFTY----N	377
	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct 201	LLDRMLE-DGLQPQNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query 378	SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	436
	MI GFCCSSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	
Sbjct 260	CMINGFCSSGRWSEAQQQLQEMLERK KISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	319
Query 437	RGIITPNTITYSSMIDGFKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRID	496
	RGIITP-TITYSSMIDGFKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct 320	RGIITPSTITYSSMIDGFKQNRLDAAEHMFYLMATKGCSPDIIIFNTLIAGYCRAKRVD	379
Query 497	GMELLHEMETTGTGLADTTTYNTLIGHFYLGVGLDNAALDLQEMISSGLCPDIVTCDTLLD	556
	G++LLHEMETE GLVA+T TY TLIHF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct 380	GIKLLHEMETEAGLVANTITYTTLIGHFCQVGDLNAAQDLLQEMVSSGVCNPVNVTCTNLLD	439
Query 557	GLCDNGKLKDALEMFVKMQKSKKLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	616
	GLCDNGKLKDALEMFK MQKS K D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct 440	GLCDNGKLKDALEMFVKAMQKS KMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query 617	YEEMPHRGIVPDTITYSSMIDGLCKQSLRDEATQMFDSMGSKSFSFPNVFTTLLINGYCK	676
	YEEMPHRGIVPDTITY+S+I GLCKQSLRDEATQMFDSMGSKSFSFPNVFTTLLINGYCK	
Sbjct 500	YEEMPHRGIVPDTITYNSVIHGLCKQSLRDEATQMFDSMGSKSFSFPNVFTTLLINGYCK	559
Query 677	AGRVDGGLELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT	736
	AGRVDGGLELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEM++SGVYPDTIT	
Sbjct 560	AGRVDGGLELFCEMGRGGIVANAITYITLIGHFRKVGNINGALDIFQEMMASGVYPDTIT	619
Query 737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY	766
	IRNMLTGLWSKEELKRAVAMLELQMS+ Y	
Sbjct 620	IRNMLTGLWSKEELKRAVAMLELDLQMSVGY	649

Group 5

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found

Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query 84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct 1	MLARVCFESSSSSSVAARFFCTGSIRIHALAEKSRDGESGEAGFRGESLKLRLSGSYEIK	60
Query 142	GLEDAAIDLFSMDLRLSRPLPSVVDFCKLGMGVVVRMERPDVLVISLYQKMERKQIRCIDIYSFN	201
	GLEDAAIDLFSMDLRLSRPLPSV+DF KLMG VVRMERPDVLVISLYQKMERKQIRCIDIYSF	
Sbjct 61	GLEDAAIDLFSMDLRLSRPLPSVIDFNKLMGAVVRMERPDVLVISLYQKMERKQIRCIDIYSFT	120
Query 202	ILIKCFCSCSKLPFA LSTFGKITKGLHPPDVVTFTLLHGLCVEDRVSEALDFFHQM FET	261
	ILIKCFCSCSKLPFA LSTFGK+T KLGHPDVVTFTLLHGLC++ RVSEALD FHQ+	
Sbjct 121	ILIKCFCSCSKLPFA LSTFGKLTKGLHPPDVVTFTLLHGLCLDHHRVSEALDLFHQI---	177
Query 262	TCRPNVVTFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	321
	CRP+V+TFTTLMNGLCREGR+VEAVALDRM+E+GLQP QITYGT VDG MCK GDTVSA	
Sbjct 178	-CRPDVLTFTTLMNGLCREGRVVEAVALDRMVENGQLQPDQITYGTIVDGMCKKGDTVSA	236
Query 322	LNLLRKMEEVSHIIIPNVVIYSAIDSLCKDGRHSDAQNLTEMQEKGIFPDLF TYNSMIV	381
	LNLLRKMEEVSHIIPNVVIYSAIDLCKDGRHS+ NLF EMQ+KGIFP++ TYN MI	
Sbjct 237	LNLLRKMEEVSHIIPNVVIYSAIDGLCKDGRHS DHNLPIEMQDKGIFPNIVTYNCMIG	296

Group 5

Query	382	GFCSSGRWSDAEQLLQEMLERKISPDVVVTYNAFVKEGKFFEAEELYDEMLPRGIIP	441
Sbjct	297	GFCISGRWSAAQRLLQEMLERKISPNVVVTYNAFVKEGKFFEAEELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSNLITFNTLIDGYCGAKRIDDGMELL	501
Sbjct	357	NTITYSSMIDGFCKQNRLDAEADMFYLMATKGCSPDVFTTTLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLVADTTTYNTLIHGFYLVGDLNAALDLQEMISSGLCPDIVTCDTLDDGLCDN	561
Sbjct	417	HEMPRRGLVANTVYTNTLIHGFCLVGDLNAALDLSQMISSGVCPDIVTCNTLDDGLCDN	476
Query	562	GKLKDALEMFKVMQSKKDLDASHIPFNGVEPDVQTYNILISGLINEGKPLEAEELYEEMP	621
Sbjct	477	GKLKDALEMFKMQSKS DLDASHIPFNGVEPDV TYNILI GLINEGKPLEAEELYEEMP	536
Query	622	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVT TLINGYCKAGRVD	596
Query	682	DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCEMGRRGIVADAIIYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMLEKLQMSMVY	766
Sbjct	657	TG WSKEL-RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1624 bits (4206), Expect = 0.0
 Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNPPIFGGLNLGVPLEGGRSRGTYSGFGLSFQFGRIGVKDFSPIRFLFLNYGSGSVRI	60
Sbjct	1	MEAPNPPIFGGLNLGVPLEGGRSRGTYSGFGLSFQFGRIGVKDFSPIRFLFLNYGSGSVRI	60
Query	61	LADSSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Query	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVDFCKLMGVVVRMERPDL	180
Sbjct	121	SCEAGFGGESLKLQSGFHEIKGLEDAIDLFSMDLRSRPLPSVVDFCKLMGVVVRMERPDL	180
Query	181	VISLYQKMERKQIRCIDIYSFNILIKCFCSCKLPFALSTFGKITKLGLHPDVVTFTLHH	240
Sbjct	181	VISLYQKMERKQIRCIDIYSFNILIKCFCSCKLPFALSTFGKITKLGLHPDVVTFTLHH	240

Group 5

Query	241	GLCVEDRVSEALDEFHQMFETTCRPNVFTTILMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDFHQMFETTCRPNVFTTILMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIIPNVVIYSAIIDLCKDGRHSDAQNL	360
Sbjct	301	TQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIIPNVVIYSAIIDLCKDGRHSDAQNL	360
Query	361	FTEMQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQLQEMLERKISPDVVTYNALINAFVK	420
Sbjct	361	FTEMQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQLQEMLERKISPDVVTYNALINAFVK	420
Query	421	EGKFEEAEEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAEHMFYLMATKGCPSPNLIT	480
Sbjct	421	EGKFEEAEEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAEHMFYLMATKGCPSPNLIT	480
Query	481	FNTLIDGYCGAKRIDGMELLHEMTETGLVADTTTYNTLIGHFYLVDLNAALDLLQEMI	540
Sbjct	481	FNTLIDGYCGAKRIDGMELLHEMTETGLVADTTTYNTLIGHFYLVDLNAALDLLQEMI	540
Query	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALLEMFVKMQSKSKLDASHPFNGVEPDVQTYNIL	600
Sbjct	541	SSGLCPDIVTCDTLLDGLCDNGKLKDALLEMFVKMQSKSKLDASHPFNGVEPDVQTYNIL	600
Query	601	ISGLINEGKFLEAEEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDMSGSKSF	660
Sbjct	601	ISGLINEGKFLEAEEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDMSGSKSF	660
Query	661	SPNVVFTTLINGYCKAGRVIDGLELFCEMGRGGIVANANITYITLICGFRKVGNINGALD	720
Sbjct	661	SPNVVFTTLINGYCKAGRVIDGLELFCEMGRGGIVANANITYITLICGFRKVGNINGALD	720
Query	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
Sbjct	721	IFQEMISSGVYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVYYWSELKRHTFQKIS	780
Query	781	GVKRCCLGVPFCSCCHHYQRQARSS 804	
Sbjct	781	GVKRCCLGVPFCSCCHHYQRQARSS 804	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against SEQ 6 from Brown provisional No. 2 (60/305,363)**

Score = 975 bits (2521), Expect = 0.0
 Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query	84	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
		MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct	1	MLARVYRSGSSSSPAVSAARLFCTRSIRHALAKKSRDG-ESGFGGESLKLRSGFHEIKGL	59

Group 5

Query	144	EDAIIDLFSMDLRSRPLPSVVFDFCKLMLGVVVRMERPDVLVISLYOKMERKQIRCDIYSFNIL	203
Sbjct	60	EDAIIDLFDM+RSRPLPSV+DFCKLMLGVVVRM R D+VISL++KME +++ C+ YSF IL	
		EDAIIDLFGDMVRSRPLPSVIDFCKLMLGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query	204	IKCFCSCSKLPFALSTFGKITKLGHLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFTTC	263
Sbjct	120	-KCFCSCSKLPFALSTFGKITKLG-----FH-----	145
Query	264	RPNVVTFTTLMNGLCREGRIVEAVALLDRMEDGLQPTQITYGTIVDGMCKKGDTVSALN P VVTF+TL+*+GLC E RI EA+ L +M+ P +T+ T+++G+C++G V A+ -PTVVFSTLLHGLCVEDRSEALDLFHQMCK---PNVVFTTLMNGLCREGRVVEAVA	323
Sbjct	146		200
Query	324	LLRKMEVSHIIPNVVIYSAIIDSLSCKDGRHSDAONLTETMQUEKG-IFPDLFY-----N	377
Sbjct	201	LLDRMLNE-DGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	378	SMIVGFCCSSGRWSDAEQLQEMLERK-ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP MI GFCCSSGRWS+A+QLQEMLERK ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	436
Sbjct	260	CMINGFCSSGRWSEAQQLQEMLERK KISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	319
Query	437	RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLNITFNTLIDGYCGAKRIDD RGIIIP+TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPL+ITFNTLI GYC AKR+DD	496
Sbjct	320	RGIIPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLDIITFNTLIAGYCRAKRVD	379
Query	497	GMELLHEMETETGLVADTTTYNTLIGHFYLVGLDNLNAALDLLQEMISSGLCPDINTCDTLL G+LLHEMTE GLVA+T TY TLIGHF VGLDNLNA DLLQEM+SSG+CE+VTC+TLD	556
Sbjct	380	GIKLLHEMETEAGLVANTITYTTLIGHFCQVGDLNAAQDLLQEMVSSGVCNPVVTCNTLLD	439
Query	557	GLCDNGKLKDALEMFVKMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL GLCDNGKLKDALEMFK MQKS D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	616
Sbjct	440	GLCDNGKLKDALEMFVKAMQKS KMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	617	YEEMPHRGIVPDITITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPPNVFTTLINGYCK YEEMPHRGIVPDITITY+S+I GLCKQSRLDEATQMFDSMGSKSFSPPNVFTTLINGYCK	676
Sbjct	500	YEEMPHRGIVPDITITYNSVIHGLCKQSRLDEATQMFDSMGSKSFSPPNVFTTLINGYCK	559
Query	677	AGRVDGGLELFCEMGRGGIVANAITYITLICFRKVGNINGALDIFQEMMISSGVYPDTIT AGRVDGGLELFCEMGRGGIVANAITYITLICFRKVGNINGALDIFQEM+SGVYPDTIT	736
Sbjct	560	AGRVDGGLELFCEMGRGGIVANAITYITLIGHFRKVGNINGALDIFQEMMASGVYPDTIT	619
Query	737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY 766	
Sbjct	620	IRNMLTGLWSKEELKRAVAMLE LQMS+ Y IRNMLTGLWSKEELKRAVAMLEDLQMSVGY 649	

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)**

Score = 523 bits (1346), Expect = 6e-146
 Identities = 262/398 (65%), Positives = 313/398 (78%), Gaps = 1/398 (0%)

Group 5

Query	371	PDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVVTYNALINAFVKEGKFFEAEEL	430
Sbjct	4	P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L PNVTTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSALNL	63
Query	431	YDEMLPRGII-PNTIITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPNLITFNTLIDGYC	489
Sbjct	64	+M I P+ + YS+-+DG K R A++F M KG P++T++ +I+G+C LRKMEELSHIKPDVVYIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFFPDIVTYSCMINGFC	123
Query	490	GAKRIDDGSELLHEMTETGLVADTTTYNTLIHGFYLGVGDLNAALDLLQEMISSGLCPDIV	549
Sbjct	124	+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V SSGKWSAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNPVV	183
Query	550	TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHIIPFNGVEPDVQTYNILISLINEGK	609
Sbjct	184	TC-TLLDGLCD GKLDKDALEM FK MQKS D-DA-HI FNGVEPDVQTYNILISLINEGK TCNTLLDGLCDRGKLKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISLINEGK	243
Query	610	FLEAEELYEEMPHIRGVIPDTITYSSMIDGLCKQSRLDEATQMFDMSGSKSFSPNVVTFTT	669
Sbjct	244	FLEAEELYEEMPHIRGVIPDT-TYSSMI+GLCKQSRLDEATQMFDMSGSKSFSPN+VTF T FLEAEELYEEMPHIRGVIPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTFNT	303
Query	670	LINGYCKAGRVDGELFCEMGRRGIVANAITYITLICFRKVGNINGALDIFQEMISSG	729
Sbjct	304	LI GYCKAG VDDGLELFCEMGRRGIVANAITYITLICFRKVGNING+LDIFQEMISSG LITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLICFRKVGNINGSLDIFQEMISSG	363
Query	730	VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSMVY	767
Sbjct	364	VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSMV + VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVF	401

Score = 394 bits (1012), Expect = 3e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query	263	CRPNVVTFTTLMNGLCREGRIVEAVALLDRMVEDGLQPQTQITYGTIVDGMCKKGDTVSAL	322
Sbjct	2	C-PNNTTFTTLMNGLCREGR-VEAVALLDRM+EDGLQP QITYGTIVDGMCK GDTVSAL CKPNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSAL	61
Query	323	NLLRKMEESHIPIVVIYSAIIDSLLDGRHSQAIDNLTEMQEKIGIFPDLFTYNSMIVG	382
Sbjct	62	NLLRKMEESHI PI+VVIYSAIIDL D KDRH+DAQNL EMQ+KGIFPD+ TY+ MI G NLLRKMEELSHIKPDVVYIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFFPDIVTYSCMING	121
Query	383	FCSSGRWSDAEQLQEMLERKISPDVVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPN	442
Sbjct	122	FCSSGRWSAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNP FCSSGKWSAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNP	181
Query	443	TITYSSMIDGFCKQNRLDAAEHMFYLM-----ATKGCPNLITFNTLIDGYCGA	491
Sbjct	182	+T +++DG C + +L A MF M A G P++ T-N LI G VVTCTNLLDGLCDRGKLKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISLINE	241
Query	492	KRIDDGSELLHEMTETGLVADTTTYNTLIHGFYLGVGDLNAALDLLQEMISSGLCPDIVTC	551
Sbjct	242	+ + EL EM G+V DT TY++I+G L+ A + M S P+IVT GKFLEAEELYEEMPHIRGVIPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTF	301

Group 5

Query 552 DTLLDGLCDNGKLKDALEMFVKVQSKKDLASHPFNGVEPDVQTYNIIISGLINEGKF 611
 +TL+ G C G + D LE+F M + G+ + TY LI G G
 Sbjct 302 NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYITLIRGFRKVGNIN 350

Query 612 EAEEELYEEMPHRGIVPPDTITYSSMIDGLCKQSRLEATQMFDSM 655
 + ++++EM G+ PDTIT +M+ GL + L A M + +
 Sbjct 351 GSLDIFQEMISSGVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394

Score = 300 bits (767), Expect = 8e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query 230 PDVVTTTLLHGLCVERDRVSEALDFHQMFFETTCRPNVVTFTLMNGLCREGRIVEAVAL 289
 P+VVTFTTL+GLC E RV EA+ +M E +PN +T+ T++G+C+ G V A+ L
 Sbjct 4 PNVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSALNL 63

Query 290 LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDL 348
 L +M E ++P + Y I=DG+ K G A NL +M++ I P++V YS +I+
 Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF 122

Query 349 CKDGRHSIDAQNLFTEMQEKGJFPDLFTYNSMIVGFCSGRWSDAEQLQEMLE----- 401
 C G+ S=AQ L EM + I PD+ T++ +I G + A+ LLQEM+
 Sbjct 123 CSSGKWSAQRLQEMLVRKISPDVVTFTSGLINALVKEGDLNSAQDLLQEMISSGVCPNV 182

Query 402 -----RKISPDVVTYNAFKEG 422
 + PDV TYN LI+ + EG
 Sbjct 183 VTCNTLLDGLCDRGKLKDALEMFVKAMQKSMMIDATHAFNGVEPDVQTYNIIISGLINEG 242

Query 423 KFFEAEELYDEMLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPLITFN 482
 KF EAEELY-EM RGI+P+T+TYSSMI+G CKQ+RDL A MF M +K SPN++TFN
 Sbjct 243 KFLEAEELYEEMPHRGIVPPDTVTYSSMINGLCKQSRLEATQMFDSMSGSKSFSPNIVTFN 302

Query 483 TLIDGYCGAKRIDDGMELLHEMETTGTGLVADTTTYNTLIGHFYLVDLNAAADDLQEMISS 542
 TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS
 Sbjct 303 TLITGYCKAGMVDDGLELFCEMGRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS 362

Query 543 GLCPDIVTCDTLLDGLCDNGKLKDALEMFVKVQKS 577
 G+ PD +T +L GL +LK AL M + +Q S
 Sbjct 363 GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS 397

Score = 216 bits (551), Expect = 8e-54
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Query 160 PSVVFCKLMGVVRMERMFDLVLISLYQKMERKQIIRCIDIYSFNILIKCFCSKLPFALST 219
 P+VV F LM + R R + +L +M + + + + + C AL+
 Sbjct 4 PNVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSALNL 63

Query 220 FGKITKLG-LHPDVVTFTTLLHGLCVERDRVSEALDFHQMFFETTCRPNVVTFTLMNGLC 278
 K+ +L + PDVV + + + GL + R ++A + F +M + P++VT++ + +NG C
 Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFC 123

Group 5

Query 279 REGRIEAVALLDRMMEDGLOPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV 338
 G+ EA LL M+ + P +T+ +++ + K+GD SA +LL+M S + PNV
 Sbjct 124 SSGKWSAQRLLQEMLVORKISPDVVTFSGLINALVKEGDLNSAQDLQEMIS-SGVCPNV 182

Query 339 VIYSAIIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDLFYTYSMIVGFCSSG 387
 V + ++D LC G+ DA +F MO+ G+ PD+ TYN +I G + G
 Sbjct 183 VTCNTL LDGLCDRGK LKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLINEG 242

Query 388 RWSDAELLQEMLERKISPDVVTYTNALINAFAVKEGKFEEAEELYDEMLPRGIIPNTITYS 447
 ++ +AE+L +EM R I PD VTY + + +IN K+ EA ++D M + PN +T++
 Sbjct 243 KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN 302

Query 448 SMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFTNLIDGYCGAKRIDDGMELLHEMTET 507
 ++ +I G+C K +D +F M +G N IT+ TLI G+ I+ +++ EM +
 Sbjct 303 TLITGYCKAGMVDDGLELFCEMGRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS 362

Query 508 GLVADTTTYNTLIGHGYLVGDLNAALDLLQEM 539
 G+ DT T + + G+ +L AL +L+E+
 Sbjct 363 GVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394

Score = 193 bits (491), Expect = 8e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query 145 DAIDLFSMDLRSRPLPSVVFDCKLGMVVVRMERPDVLVISLYQKMER-KQIRCDIYSFNIL 203
 +A+ L M+ P+ + + ++ +M ++L +KME I+ D+ ++ +
 Sbjct 24 EAVALLDRMVEDGLQPQITYGTIVDGMCKKGDTVSALNLLRKMEELSHIKPDVVIYSAI 83

Query 204 IKCFCSCSKLPFALSTFGKITKGLHLPDVFTTLLHGLCVEDRVSEALDDFHQMFTTC 263
 I + A + F ++ G+ PD+VT++ +++G C + SEA +M
 Sbjct 84 IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSCMINGFCSSGKWSAQRLLQEMLVRKI 143

Query 264 RPNVFTTLMNGLCREGRIEAVALLDRMMEDGLOPTQITYGTIVDGMCKKGDTVSALN 323
 P+VTF+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL
 Sbjct 144 SPDVVTFSGLINALVKEGDLNSAQDLQEMISSGVCNPVNTCNCNDLGLCDRGK LKDALE 203

Query 324 LLRKME-----EVSH----IIPNVVIIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPD 373
 + + M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD
 Sbjct 204 MFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLINEGKFLAEELYEEMPHRGIVPD 263

Query 374 FTYSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYTNALINAFAVKEGKFEEAEELYDE 433
 TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E
 Sbjct 264 VTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNLTITGYCKAGMVDDGLELFCE 323

Query 434 MLPRGIIPNTITYSSMINGFCKQNRLDAAEHMFYLMATKGCSPNLITFTNLIDGYCGAKR 493
 M RGE+ N ITY + +I GF K + + + F M + G P+ IT + + G +
 Sbjct 324 MGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSGVPDTITIRNMLTGLWSKEE 383

Query 494 IDDGMELLHEM 504
 + + +L E+
 Sbjct 384 LKRALAMLEEL 394

Group 5

Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query	135	SGFEHKLEDAIDLFSMDLRSRPLPSVVFCKLMGVVRMERPDLVISLYQKMERKQIR	194
	+GF	+A L +ML + P VV F L+ +V+ + L Q+M +	
Sbjct	120	NGFCSSGKWSEAQRLQEMVLVRKISPWTFTSGLINALVKEGDLNSAQDLQEMISSGVC	179
Query	195	CDIYSFNILIKCFCSCSKLPFALSTFGKITL-----GLHPDVVTFTLLHGLC	243
	++ + N L+ C KL AL F + K	G+ PDV T+ L+ GL	
Sbjct	180	PNVVTCNTLLDGLCDRGKLKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLI	239
Query	244	VEDRVSEALDFFFHQMFETTCRPNVVTFTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI	303
	E + EA ++ +M P+ VT+++++NGLC++ R+ EA + D M P +		
Sbjct	240	NEGKFLEAAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIV	299
Query	304	TYGTIVDGMCKKGDTVSALNLLRKMEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFT	363
	T+ T++ G CK G L L -M I+ N + Y +I K G + + ++F E		
Sbjct	300	TFNTLITGYCKAGMVDGLELFCEMGRGG-IVANAITYITLIRGFRKVGNINGSLIFQE	358
Query	364	MQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQQLQEMLERKIS	405
	M G++PD T +M+ G S A +L+E+ +S		
Sbjct	359	MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS	400

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 5

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found

Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1180 bits (3053), Expect = 0.0

Identities = 595/685 (86%), Positives = 629/685 (91%), Gaps = 6/685 (0%)

Query 84	MLARVCGFKCSSSPAESAARLFCTRISRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	141
	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct 1	MLARVCRFESSSSSSVSAARFFCTGSIRHALAEKSRSRDGESGEAGFRGESLKLRSGSYEIK	60
Query 142	GLEDAIDLFSMDLRLSRPLPSVDFCKLMGVVVRRMERPDVLVISLYQKMERKQIRCIDIYSFN	201
	GLEDAIDLFSMDLRLSRPLPSV+DF KLMG VVRMERPDVLVISLYQKMERKQIRCIDIYSF	
Sbjct 61	GLEDAIDLFSMDLRLSRPLPSVIDFNKLGMGAVVRRMERPDVLVISLYQKMERKQIRCIDIYSFT	120
Query 202	ILIKCFCSCKLPFALSTFGKITKLGHLIPDVVTFTTLHGLCVEDRVSSEALDFFHQMFFET	261
	ILIKCFCSCKLPFALSTFGK+TKLGLIPDVVTFTTLHGLC++ RVSEALD FHQ+	
Sbjct 121	ILIKCFCSCKLPFALSTFGKLTKLGHLIPDVVTFTTLHGLCLDHVRSEALDLFHQI---	177
Query 262	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQLPTQITYGTIVDGMCKGDTVSA	321
	CRP+V-TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMC K GDTVSA	
Sbjct 178	-CRPDVLTFPTTLMNGLCREGRVVEAVALLDRMVENGQLQPDQITYGTVDGMCKMGDTVSA	236

Group 5

Query	322	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFTYNMSIV	381
Sbjct	237	LNLLRKMEE-SHI PNVVIYSAIID LCKDGRHS+ NLF EMQ+KGIFP++ TYN MI	296
Query	382	GFCSSGRWSDAEQLLQEMLERKISPVVVTYNALINAFVKEGKFFEAELYDEMLPRGIIP	441
Sbjct	297	GFC SGRWS A+-LLQEMLERKISP+VVVTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	356
Query	442	NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPNLTIFNTLIDGYCGAKRIDDGMELL	501
Sbjct	357	NTITY-SMIDGFCKQ+RLDAAE MFYLMATKGCP++ TF TLIDGYCGAKRIDDGMELL	416
Query	502	HEMTETGLVADTTTYNTLIGHFYLGVGDNAALDLQEMISSGLCPPIVTCDTLLDGLCDN	561
Sbjct	417	HEM GLVA-T TYNTLIGHF LVGDINAALDL Q+MISSG-CPDIVTC+TLGDGLCDN	476
Query	562	GKLKDALEMFKVMQSKKKLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP	621
Sbjct	477	GKLKDALEMFKMOKSK DLDASHPFNGVEPDV TYNIL GLINEGKFLEAEELYEEMP	536
Query	622	HRGIVPDITYYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVTFTTLINGYCKAGRVD	681
Sbjct	537	HRGIVPDITYYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVTF TLINGYCKAGRVD	596
Query	682	DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	741
Sbjct	597	DGLELFCEMGRRGIVADAIIYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	656
Query	742	TGLWSKEELKRAVAMELK LQMSMVY	766
Sbjct	657	TG WSKEL-RAVAMLE LQMS+ Y	681

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1624 bits (4206), Expect = 0.0
 Identities = 804/804 (100%), Positives = 804/804 (100%), Gaps = 0/804 (0%)

Query	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGFSSLFGFRIFGVKDFSPIRFLFLNYGSGSVRI	60
Sbjct	1	MEAPNYPIFFGLNLGVPLEGGRSGTYSFGFSSLFGFRIFGVKDFSPIRFLFLNYGSGSVRI	60
Query	61	LADSSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120
Sbjct	61	LADSSRVFFDRRRRTKFRRNKNKMLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGE	120

Group 5

Query	121	SCEAGF GGESLKLQSGFHEIKGLEDAIDLFSMLRSRPLPSVVD FCKLMGVVV RMERPD L	180
Sbjct	121	SCEAGF GGESLKLQSGFHEIKGLEDAIDLFSMLRSRPLPSVVD FCKLMGVVV RMERPD L	180
Query	181	VISLYQKMERKQIRC D IYSFNILIKCFCSCSKLPF ALSTFGKITKGLH PDVVFTTLLH	240
Sbjct	181	VISLYQKMERKQIRC D IYSFNILIKCFCSCSKLPF ALSTFGKITKGLH PDVVFTTLLH	240
Query	241	GLCVEDRVSEALDFHQM FETTCRPN VFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Sbjct	241	GLCVEDRVSEALDFHQM FETTCRPN VFTTLMNGLCREGRIVEAVALLDRMMEDGLQP	300
Query	301	TQITYGTIVDGMCKKG DTVSALNLLRKMEEVSHIIPN VVIYSAIIDS LCKDGRHS DAQNL	360
Sbjct	301	TQITYGTIVDGMCKKG DTVSALNLLRKMEEVSHIIPN VVIYSAIIDS LCKDGRHS DAQNL	360
Query	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLQ EMLERKISPDVVTYNA FVK	420
Sbjct	361	FTEMQEKGIFPDLFTYNSMIVGFCSSGRWSDAEQLQ EMLERKISPDVVTYNA FVK	420
Query	421	EGKF FEAEEELYDEMLPRGIIP PNTITYSSMIDGFCKQNRL DAAEHMFYLMATKG CSPN LIT	480
Sbjct	421	EGKF FEAEEELYDEMLPRGIIP PNTITYSSMIDGFCKQNRL DAAEHMFYLMATKG CSPN LIT	480
Query	481	FNTLIDGYCGAKRIDGMELLHEMTETGLVADTT YNTL IHGFYLVGD LNAALD LQEMI	540
Sbjct	481	FNTLIDGYCGAKRIDGMELLHEMTETGLVADTT YNTL IHGFYLVGD LNAALD LQEMI	540
Query	541	SSGLCPD IVCTD LLDGLCDNGKL KDALEMFKV MOKSKKD L DASHPFNGVEPDV QTYN IL	600
Sbjct	541	SSGLCPD IVCTD LLDGLCDNGKL KDALEMFKV MOKSKKD L DASHPFNGVEPDV QTYN IL	600
Query	601	ISGLINEGKFLEAEEELYEEMPHRGIVPPDTITYSSMID GLCKQS RLDEATQ MFDSM GS KSF	660
Sbjct	601	ISGLINEGKFLEAEEELYEEMPHRGIVPPDTITYSSMID GLCKQS RLDEATQ MFDSM GS KSF	660
Query	661	SPNVFTTTLINGYCKAGR VDDGLELFCEMGR RGIVANA ITYITLICGFRKVGN INGAL D	720
Sbjct	661	SPNVFTTTLINGYCKAGR VDDGLELFCEMGR RGIVANA ITYITLICGFRKVGN INGAL D	720
Query	721	IFQEMI SSGVYPDTITIRNMLTGLWSKEELKRAVAM LEKLQMSMVYYWSELKRHTFQK IS	780
Sbjct	721	IFQEMI SSGVYPDTITIRNMLTGLWSKEELKRAVAM LEKLQMSMVYYWSELKRHTFQK IS	780
Query	781	GVKRCCLGVC PFCSC HGHYRQARSS	804
Sbjct	781	GVKRCCLGVC PFCSC HGHYRQARSS	804

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)

Group 5

Score = 975 bits (2521), Expect = 0.0
 Identities = 511/690 (74%), Positives = 569/690 (82%), Gaps = 48/690 (6%)

Query 84	MLARVCGFKCSSSPAESAARLFCTRDIRTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143
	MLARV SSSPA SAARLFCTRIR LAK S + E+GFGGESLKL+SGFHEIKGL	
Sbjct 1	MLARVYRSGSSSSPAVAESAARLFCTRIRHALAKSRDG-ESGFGGESLKLRSGFHEIKGL	59
Query 144	EDAIDLFSDMLRSRPLPSVVDFCKLMGVVVRMERPDVLVISLYQKMERKQIRCIDIYSFNIL	203
	EDAIDLF DM+RSPRLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	
Sbjct 60	EDAIDLFGDMVRSRPLPSVIDFCKLMGVVVRMGRLDVVISLHRKMEMRRVPCNAYSFTIL	119
Query 204	IKCFCSCSKLPALSTFGKITKLGLHPDVVTFTLLHGLCVEDRVSEALDDFHQMFTTC	263
	+KCFCSCKLPALSTFGKITKLG FH	
Sbjct 120	MKCFCSCKLPALSTFGKITKLG----- FH-----	145
Query 264	RPNVVTFTTLMNGLCREGRIVEAVALLDRRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
	P VVT+CL+ +GLC E RI AE + L +M + P +T+ T+++G+C++G V A+	
Sbjct 146	-PTVVFTSTLLHGLCVEDRIVESEALDDLFHQMCK---PNVVTFTTLMNGLCREGRVVEAVA	200
Query 324	LLRKMEEVSHIIPNVVIYSAIIDSCLKDGRHSDAQNLFTEMQEKG-I FPDLFTY----N	377
	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ +	
Sbjct 201	LLDRMLE-DGLQPQNQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query 378	SMIVGFCSSGRWSDAEQLLQEMLERK-ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	436
	MI GFCCSSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	
Sbjct 260	CMINGFCSSGRWSEAQQQLQEMLERK KISPDVVTYNALINAFVKEGKFEEAEELYDEMLP	319
Query 437	RGIITPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPNLITFNTLIDGYCGAKRID	496
	RGIITP-TITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSP++ITFNTLI GYC AKR+DD	
Sbjct 320	RGIITPSTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSPDIIIFNTLIAGYCRAKRVD	379
Query 497	GMELLHEMETTGTGLADTTTYNTLIGHFYLGVGLDNAALDLQEMISSGLCPDIVTCDTLLD	556
	G++LLHEMETE GLVA+T TY TLIHF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD	
Sbjct 380	GIKLLHEMETEAGLVANTITYTTLIGHFCQVGDLNAAQDLLQEMVSSGVCNPVNVTCTNLLD	439
Query 557	GLCDNGKLKDALEMFVKMQKSKKLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	616
	GLCDNGKLKDALEMFK MQKS K D+DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	
Sbjct 440	GLCDNGKLKDALEMFVKAMQKS KMDIDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query 617	YEEMPHRGIVPDTITYSSMIDGLCKQSRLEATQMFDMSMGSKSFSPNVTFTTLINGYCK	676
	YEEMPHRGIVPDTITY+S+I GLCKQSRLEATQMFDMSMGSKSFSPNVTFTTLINGYCK	
Sbjct 500	YEEMPHRGIVPDTITYNSVIHGLCKQSRLEATQMFDMSMGSKSFSPNVTFTTLINGYCK	559
Query 677	AGRVDGGLELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT	736
	AGRVDGGLELFCEMGRGGIVANAITYITL I GFRKVGNINGALDIFQEM++SGVYPDTIT	
Sbjct 560	AGRVDGGLELFCEMGRGGIVANAITYITLIGHFRKVGNINGALDIFQEMMASGVYPDTIT	619
Query 737	IRNMLTGLWSKEELKRAVAMLEKLQMSMVY 766	
	IRNMLTGLWSKEELKRAVAMLEL QMS+ Y	
Sbjct 620	IRNMLTGLWSKEELKRAVAMLELDLQMSVGY 649	

Group 5

- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found

Group 5

- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from April 2001 (JP 2001-128008) against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 1 from Brown provisional No. 1 (60/305,026)**

Score = 521 bits (1341), Expect = 2e-145

Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query 288	PDLFTYNSMIVGFCSSGRWSAEQLLQEMLERKISPDVVVTYNALINAFVKEGKFFEAEEL	347
	P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct 4	PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQIYTGTIVDGMCKMGDTVSALNL	63
Query 348	YDEMPLRGGII-PNTITYSSMIDGFCKQNRLDAEHHMFYLMATKGCPSPNLITFNTLIDGYC	406
	+M I P+ YS++IDG K R A+++F M KG P+++T++ +I+G+C	
Sbjct 64	LRKMEELSH7KPDVVIYSAIIDGLWKDGHRHTDAQNLFIEMQDKGIPFDIVTYSCMINGFC	123
Query 407	GAKRIDDGMEILLHEMTETGLVADTTTNTLIHGFYLVGDLNAALDLLQEMISSGLCPDIV	466
	+ + + LL EM + D T++ LI+ GDLN+A DLLQEMISSG+CP++V	
Sbjct 124	SSGKWSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCNVV	183
Query 467	TCDTLLDGLCDNGKLKDALEMFKVMQKSKKDLDASHPFGVEPDVQTYYNILISGLINEGK	526
	TC+TLLDGLCDNGKLKDALEMFK MQKS D+DA+H FNGVEPDVQTYYNILISGLINEGK	
Sbjct 184	TCNTLLDGLCDRGKLKDALEMFKAMQKSMMID1DATHAFNGVEPDVQTYYNILISGLINEGK	243
Query 527	FLEAAELYEEMPHRGIVPDPTITYSSMIDGLCKQSRLDEATQMFDMSGSKSFSPNVTFTT	586
	FLEAAELYEEMPHRGIVPDPT+TYSSMI+GLCKQSRLDEATQMFDMSGSKSFSPN+VTF T	
Sbjct 244	FLEAAELYEEMPHRGIVPDVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTFNT	303

Group 5

Query 587 LINGYCKAGRVDGGLELFCEMGRGIVANAITYITLICGFRKVGNINGALDIFQEMISSG 646
 LI GYCKAG VDDGLELFCEMGRGIVANAITYITLI GFRKVGNING+LDIFQEMISSG
 Sbjct 304 LITGYCKAGMVDDGLELFCEMGRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSG 363

Query 647 VYPDTITIRNMLTGLWSKEELKRAVAMLEKLQMSM 681
 VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM
 Sbjct 364 VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM 398

Score = 394 bits (1012), Expect = 2e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query 180 CRPNVVTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCCKGDTVSAL 239
 C+PNNVFTTLMNGLCREGR-VEAVALDRM+EDGLQP QITYGTIVDGMCCK GDTVSAL
 Sbjct 2 CKPNVVTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCCKGDTVSAL 61

Query 240 NLLRKMEEVSHIIPNVIYSAIIDSLCKDGRHISDAQNLFTEMQEKGIFPDFTYNSIMIVG 299
 NLLRKME+SHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G
 Sbjct 62 NLLRKMEELSHIKPDVVIYSAIIDGLWKGDRHTDAQNLFIEMQDKGIFPDIVTYSCMING 121

Query 300 FCSSGRWSDAEQLQEMLERKISPDVVTYNALINAFVKEGKFFEAEELYDEMLPRGIIPN 359
 FCSSG-WS+A+-+LQEML RKISPDV++ LINA VKEG A++L EM+ G+ PN
 Sbjct 122 FCSSGKWSSEAQLQEMLVMVRKISPDVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCN 181

Query 360 TITYSSMIDGFCQKNRLDAABHMFYLM-----ATKGSPNLTFTNLIDGYCGA 408
 +T +--+DG C + +L A MF M A G P++ T+N LI G
 Sbjct 182 VVTCTNTLLDGLCDRGKLKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLINE 241

Query 409 KRIDDGMELLHEMTETGLVADTTTNTLIHGFLVGDLNAAALDLLQEMISSGLCPDIVTC 468
 + + EL EM G+V DT TY++I+G L+ A + M S P+IVT
 Sbjct 242 GKELEAEELYEEMPHIRGIVPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTF 301

Query 469 DTLLDGLCDNGKLKDALEMFVKMQKSKKLDASHPFNGVPEPDVQTYNILISGLINEKGFL 528
 +TL+ G C G + D LE+F M + G+ + TY LI G G
 Sbjct 302 NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYITLIRGFRKVGNN 350

Query 529 EAEELYEEMPHRGIVPDTITYSSMINGLCKQSRLDEATQMFDMSG 572
 + +--+EM G+ PDTIT +M+ GL + L A M + +
 Sbjct 351 GSLDIFQEMISSGVPDTITIRNMLTGLWSKEELKRALAMLEEL 394

Score = 300 bits (767), Expect = 6e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query 147 PDVVTTLLHGLCVEDRVSEALDDFFHQMFETTCRPNVFTTLMNGLCREGRIVEAVAL 206
 P+VVTFTT+GLC E RV EA +M E +PN +T+ T++G+C+ G V A+ L
 Sbjct 4 PNVVTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPNQITYGTIVDGMCCKGDTVSALNL 63

Query 207 LDRMME-DGLQPTQITYGTIVDGMCCKGDTVSALNLLRKMEEVSHIIPNVVIYSAIDL 265
 L +M E ++P + Y I+DG+ K G A NL +M++ I P++V YS +I+
 Sbjct 64 LRKMEELSHIKPDVVIYSAIIDGLWKGDRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF 122

Group 5

Query	266	CKDGRHSDAQNLFTEMQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLE-----	318
	C	G+ S+AQ L EM + I PD+ T++ +I G + A+ LLQEM+	
Sbjct	123	CSSGKWNSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLSAQDLLQEMISSGVCPNV	182
Query	319	-----RKISPDPVVTTYNALINAFVKEG + PDV TYN LI+ + EG	339
Sbjct	183	VTCNTL LDGLCDRGKLKDALLEMFKA MKQSMMIDAT HAFNGVEPDVQTYN ILISGLINEG	242
Query	340	KFFEAEELYDEMLPRGIIPNITYSSMIDGFCKQNRLDAEHMFYLMATKGCSPNLITFN	399
	KF	EAEELY-EM RQI+P+T+TYSSMI+G CKQ+RLD A MF M +K SPN++TFN	
Sbjct	243	KFLEAEELYEEMPHRGIVPDVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN	302
Query	400	TLIDGYCGAKRIDDGMELLHEMTTGVLADTTTNTLHGFYLVGDLNAA LDLLQEMISS	459
	TLI	GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS	
Sbjct	303	TLITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS	362
Query	460	GLCPDIVTCDTL LDGLCDNGKLKDALLEMFKVMQKS 494	
	G+	PD +T +L GL +LK AL M + +Q S	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLELOMS 397	
Score = 216 bits (551), Expect = 7e-54			
Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)			
Query	77	PSVVFCKLGMGVVRRMERPDVLVISLYQKMERQKIRCDIYSFNILIKCFCSCSKLPFALST	136
	P+VV F	LM + R R ++L +M ++ + ++ ++ C AL+	
Sbjct	4	PNVVTFTTLMGLCREGRVVEAVALLDRMVEDGLQPNCQITYGTIVDGMCKMGTDSALNL	63
Query	137	FGKITKLG-LHPDVTTFTLLHGLCVDRVS EALDFFFHQMFETTCRPNVVTFTLMGLC	195
	K+	+L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	
Sbjct	64	LRKMEELSHIKPDPVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPPDIVTYSCMINGFC	123
Query	196	REGIVEAVALLRNMEDGLQPTQITYTIVDGMCKKGDTSALNLLRKMEEVSHIIIPNV	255
	G+	EA LL M+ + P +T+ ++ + K+GD SA +LL+ +M S + PNV	
Sbjct	124	SSGKWNSEAQRLLQEMLVRKISPDVVTFSGLINALVKEGDLSAQDLLQEMISS-SGVCPNV	182
Query	256	VIYSAIIDSLCKDGRHSDAQNLFTEMQE-----KGIFPDLFYTNSMIVGFCSSG	304
	V	+ ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G	
Sbjct	183	VTCNTL LDGLCDRGKLKDALLEMFKA MKQSMMIDAT HAFNGVEPDVQTYN ILISGLINEG	242
Query	305	RWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFEEAELYDEMLPRGIIPNITYS	364
	++ +AB+L +EM R I PD VTY++ +IN K+ + EA ++ +D M + PN +T++		
Sbjct	243	KFLEAEELYEEMPHRGIVPDVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFN	302
Query	365	SMIDGFCKQNRLDAEHMFYLMATKGCSPNLITFTNLIDGYCGAKRIDDGMELLHEMT	424
	++I G+CK	+D +F M +G + I+ +++ EM +	
Sbjct	303	TLITGYCKAGMVDDGLELFCEMGRGGIVANAITYITLIRGFRKVGNINGSLDIFQEMISS	362
Query	425	GLVADTTTNTLHGFYLVGDLNAA LDLLQEM 456	
	G+	DT T ++ G + +L AL +L+E+	
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEEL 394	

Group 5

Score = 193 bits (491), Expect = 6e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query 62	DAIDLFSMLRSRPLPSVVDCKLMGVVVRMERPDLVISLYQKMER-KQIRC迪YSFNIL	120
+A- L M+	P+ + + ++ + +M	++L -KME I+ D+ ++ +
Sbjct 24	EAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGKDTVSALNLLRKMEELSHIKPDPVVIYSAI	83
Query 121	IKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTLLHGLCVEDRVSEALDFFHQMFFETTC	180
I + A + F ++ G+ PD+VT++ +++G C + SEA +M		
Sbjct 84	IDGLWKDGRHTDAQNLIFIEMQDKGJIFPPDIVTYSCMINGFCSSGKWSSEAQRLLQEMLVRKI	143
Query 181	RPNVVFPTTLMNGLCREGRIVEAVALLDRMEDGLQOPTQITYGTIVDGMCKKGDTVSALN	240
P+VVT� L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL		
Sbjct 144	SPDVVFSGLINALVKEGDLNSAQDLQEMISSGVCNPVNTCTNLLDGLCDRGKLKDALE	203
Query 241	LLRKME-----EVSH---IIPNVVIIYSAIIDSCLKDGRHSADAQNLFTEMQEKGJIFPDL	290
+ + M+ + +H + P-V Y+ +I L +G+ +A+ L+ EM +GI PD		
Sbjct 204	MFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHRGIVPDT	263
Query 291	FTYNSMIVGFCSSGRWSDAEQLLQEMLERKISPVDTVVYNALINAFVKEKGKFEEAEELYDE	350
TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E		
Sbjct 264	VTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE	323
Query 351	MLPRGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGKSPNLTIFTNLITDGYCGAKR	410
M RGI+ N ITY ++I GF K ++ + +F M + G P+ IT ++ G +		
Sbjct 324	MGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSGVPDTITIRNMLTGLWSKEE	383
Query 411	IIDDGMELLHEM 421	
+ + +L E+		
Sbjct 384	LKRALAMLEEL 394	

Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query 52	SGFHEIKGLEDAIDLFSMLRSRPLPSVVDCKLMGVVVRMERPDLVISLYQKMERQIR	111
+GF +A L +ML + P VV F L+ +V+ + L Q+M +		
Sbjct 120	NGFCSSGKWSSEAQRLLQEMLVRKISPDVVTFTSGLINALVKEGDLNSAQDLQEMISSGVC	179
Query 112	CDIYSFNILIKCFCSCKLPFALSTFGKITKL-----GLHPDVVTFTLLHGLC	160
++ + N L+ C KL AL F + K G+ PDV T+ L+ GL		
Sbjct 180	PNVVTCTNLLDGLCDRGKLDALEMFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISGLI	239
Query 161	VEDRVSEALDFFHQMFFETTCRPNVVTFTLMNGLCREGRIVEAVALLDRMEDGLQOPTI	220
E + EA + + +M P+ VT+++++NGLC++ R+ EA + D M P +		
Sbjct 240	NEGKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFSPNIV	299

Group 5

Query 221 TYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNVVIYSAIIDLCKDGRHSDAQNLFTTE 280
T+ T++ G CK G L L +M I+ N + Y +I K G + + ++F E
Sbjct 300 TFNTLTGYCKAGMVDDGLELFCEMGRGG-IVANAITYITLIRGFRKVGNINGSLDIFQE 358

Query 281 MQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQLLQEMLERKIS 322
M G++PD T +M+ G S A +L+E+ +S
Sbjct 359 MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS 400

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 6 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 7 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 8 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 9 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 10 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 11 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 12 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 13 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 14 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 15 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 16 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 17 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 18 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 19 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 20 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 21 from Brown provisional No. 1 (60/305,026)
 - No significant similarity was found

Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 22 from Brown provisional No. 1 (60/305,026)**

Score = 1179 bits (3049), Expect = 0.0
 Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query 1	MLARVCGFCKCSSSPAESAARLFCTRSIRDTLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
Sbjct 1	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	60
Query 59	GLEDAIDLFSMDLRSRPLPSVWDFCKLMGVVVVRMERPDLVISLYQKMERKQIRCIDIYSFN	118
Sbjct 61	GLEDAIDLFSMDLRSRPLPSVWDFCKLMGVVVVRMERPDLVISLYQKMERKQIRCIDIYSFT	120
Query 119	ILIKCFCSCSKLPFALSTFGKITKLGLHPDVVTFTTLHGLCVEDRVSEALDFFHQMFET	178
Sbjct 121	ILIKCFCSCSKLPFALSTFGK+TKLGLHPDVVTFTTLHGLC++RVSEALD FHQ+	177
Query 179	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
Sbjct 178	CRP+V+TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCK GDTVSA	236
Query 239	LNLRLRMEEVSHIIPNVVIYSAIIDSCLKDGRHSDAQNLFTEMQEKGIFPPDLFTYNSMIV	298
Sbjct 237	LNLRLRMEEVSHIIPNVIYSAIIDLGLCDGRHSDHNLFIEMQDKGIFPNIVTYNCMIG	296
Query 299	GFCSSGRWSDAEQLLQEMLERKISPDVVNTYNALINAFVKEGKFEEAELYDEMLPRGIIP	358
Sbjct 297	GFC SGRWS A+-LLQEMLERKISP+VVTYNAFVKEGKFEEAELYDEMLPRGIIP	356
Query 359	NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGKCPSPNLITFNTLIDGYCGAKRIDDGMELL	418
Sbjct 357	NTITY+SMIDGFCKQ+RLDAAE MFYLMATKGKSP++ TF TLIDGYCGAKRIDDGMELL	416
Query 419	HEMTETGLVADTTTNTLIGHFYLGVGDLNAA LDLLQEMISSGLCPDIVTCDTLLGLCDN	478
Sbjct 417	HEMPRGLVANTVTNTLIGHFCLVGDLNAA LDLSQQMISSGVPDPDIVTCNTL LDGLCDN	476
Query 479	GKLKDALEMFKVMQSKKKLDASHPFNGVPEVDVQTYNLIISGLINEGKFLEAEELYEEMP	538
Sbjct 477	GKLKDALEMFK MQSK DLDASHPFNGVPEPDV TYNILI GLINEGKFLEAEELYEEMP	536
Query 539	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD	598
Sbjct 537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSPNVVT FTTLINGYCKAGRVD	596
Query 599	DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	658
Sbjct 597	DGLELFCEMGRRGIVADAIIYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNML	656

Group 5

Query 659 TGLWSKEELKRAVAMLEKLQMSM 681
 TG WSKEL+RAVAMLE LQMS+
 Sbjct 657 TGFWSKEELERAVAMLEDLQMSV 679

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 23 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 24 from Brown provisional No. 1 (60/305,026)**

Score = 1368 bits (3541), Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query 1	MLARVCGFCKSSSPAESAARLFCTRSIRDTLAKASGESCEAGF GGESLKLQSGFHEIKGL	60
Sbjct 84	MLARVCGFCKSSSPAESAARLFCTRSIRDTLAKASGESCEAGF GGESLKLQSGFHEIKGL	143
Query 61	EDAIIDLFSMDMLRSRPLPSVVDFCKLGMVVVRMERPDVLVISLYQKMERKQIRCEDIYSFNIL	120
Sbjct 144	EDAIIDLFSMDMLRSRPLPSVVDFCKLGMVVVRMERPDVLVISLYQKMERKQIRCEDIYSFNIL	203
Query 121	IKCFCCSKLKFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFFETTC	180
Sbjct 204	IKCFCCSKLKFALSTFGKITKLGLHPDVVTFTTLLHGLCVEDRVSEALDFFHQMFFETTC	263
Query 181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
Sbjct 264	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	323
Query 241	LLRKMEEVSHIIIPNVVIYSAIIDSCLKDGRHSDAQNLTEMQEKGIFPPDLFTYNSMIVGF	300
Sbjct 324	LLRKMEEVSHIIIPNVVIYSAIIDSCLKDGRHSDAQNLTEMQEKGIFPPDLFTYNSMIVGF	383
Query 301	CSSGRWSDAEQLLOEMLERKISPDVVTYNALINAFVEKGFFEAEELYDEMLPRGIIPNT	360
Sbjct 384	CSSGRWSDAEQLLOEMLERKISPDVVTYNALINAFVEKGFFEAEELYDEMLPRGIIPNT	443
Query 361	ITYSSMIDGFCQKNRLDAAEHMFYLMATKGCPNLTITFTNLIDGYCGAKRIDDGMELLHE	420
Sbjct 444	ITYSSMIDGFCQKNRLDAAEHMFYLMATKGCPNLTITFTNLIDGYCGAKRIDDGMELLHE	503
Query 421	MTETGLVADTTTNTLIHGFYLVGDINAALDLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct 504	MTETGLVADTTTNTLIHGFYLVGDINAALDLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query 481	LKDALEMFKVMQSKKLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
Sbjct 564	LKDALEMFKVMQSKKLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623

Group 5

Query	541	GIVPDTITYSSMIDGLCKQSRLEATQMFDMSGSKSFSPNVFTTTLINGYCKAGRVDGG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSRLEATQMFDMSGSKSFSPNVFTTTLINGYCKAGRVDGG	683
Query	601	LELFCEMGRRGIVANAINITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRRGIVANAINITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083) against PRT SEQ 25 from Brown provisional No. 1 (60/305,026)**

Score = 974 bits (2517), Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Query	1	MLARVCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
Sbjct	1	MLARV SSSPA SAARLFCTRSIR LAK S + E+GFGGESLKL+SGFHEIKGL	59
Query	61	EDAIIDLFSDMRLSRSLRPLPSVVFDCKLMLGVVVVRMERPDVLVISLYQKMERKQIRC	120
Sbjct	60	DAIIDL R+D+RSLRPLPSVVFDCKLMLGVVVVRMRGLRDVVISLHRKMEMRRVPCNAYSTIL	119
Query	121	IKCFCSCSKLPFALSTFGKITKLGHPDVVTFTLLHGLCVEDRVSEALDFFHQMFTTC	180
Sbjct	120	-KCFCSCKLPFALSTFGKITKLG-----FH-----	145
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
Sbjct	146	P VVTF+TL+GLC E RI EA+L +M + P +T+ T+++G+C++G V A+ -PTVVFSTLLHGLCVEDRIESEALDLFHQMCK---PNVVTFTTLMNGLCREGRVVEAVA	200
Query	241	LLRKMEEVSHIIIPNVVIYSAIIDSLCKDGRHSDAQNLTTEMQEKG-IFPDLFY-----N	294
Sbjct	201	LLDRMLE-DGLQPQNTQITYGTIVDGMCKMGDTVSALNLLRKMEEVSHIKPNVVIWPLERRT	259
Query	295	SMIVGFCSGRWSDAEQLLQEMLERK-ISPDVTSVNLINAFAVKEGKFFEAEEELYDEMLP	353
Sbjct	260	MI GFCSGRWS+A+QLLQEMLERK ISPDVVTYNALINAFAVKEGKFFEAEEELYDEMLP	319
Query	354	RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPNLTIFNTLIDGYCGAKRIDD	413
Sbjct	320	RGIIPNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPDIITFNTLIAGYCRAKRVD	379
Query	414	GMELLHEMTETGLVADTTTYNTLIGHGYLVGLDNAALDLLQEMISSGLCPDIVTCDTLLD	473
Sbjct	380	G++LLHEMTE GLVA+T TY TLIGHF VGDLNAA DLLQEM+SSG+CP++VTC+TLLD	439

Group 5

Query	474	GLCDNGKLKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	533
Sbjct	440	GLCDNGKLKDALEMFK MQSK D-DASHPFNGVEPDVQTYNILISGLINEGKFLEAEEL	499
Query	534	YEEMPHRGIVPDITTYSSMIDGLCKQSRLDEATQMFDMSGSKSFSPNVVTFTTLINGYCK	593
Sbjct	500	YEEMPHRGIVPDITTY-S+I GLCKQSRLDEATQMFDMSGSKSFSPNVVTFTTLINGYCK	559
Query	594	AGRVDGGLELFCEMRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTIT	653
Sbjct	560	AGRVDGGLELFCEMRRGIVANAITYITLICGFRKVGNINGALDIFQEM++SGVYPDTIT	619
Query	654	IRNMLTGLWSKEELKRAVAMLEKIQMSM	681
Sbjct	620	IRNMLTGLWSKEELKRAVAMLE LQMS+	647

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 26 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 27 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 28 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 29 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 30 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 31 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 32 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 33 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found

Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 34 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 35 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 36 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 37 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 38 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 39 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 40 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 41 from Brown provisional No. 1 (60/305,026)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against SEQ 4 from Brown provisional No. 2 (60/305,363)**

Score = 1179 bits (3049), Expect = 0.0
Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query 1	MLARVCGFKCSSSPAESAARLFCTRSLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct 1	MLARVCRFESSSSSSAARFFCTGSIRHALAEKSRSRGEAGFRGESLKLRLSGSYEIK	60
Query 59	GLEDAIDLFSMDMLRSRPLPSVVDFCKLGMGVVRMERPDVLVISLYQKMERKQIRCIDIYSFN	118
	GLEDAIDLFSMDMLRSRPLPSV+DF KLMG VVRMERPDVLVISLYQKMERKQIRCIDIYSF	
Sbjct 61	GLEDATDLFSMDMLRSRPLPSVIDFKLGMGA VVRMERPDVLVISLYQKMERKQIRCIDIYSFT	120

Group 5

Query	119	ILIKCFCSCSKLPFALSTFGKITKGLHPDVVTFTTLIHLGLCVEDRVSLEALDFHQMFE	178
Sbjct	121	ILIKCFCSCSKLPFALSTFGKITKGLHPDVVTFTTLIHLGLCVEDRVSLEALDFHQMFE	177
Query	179	TCRPNVVTTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	238
Sbjct	178	CRP+V-TFTTLMNGLCREGRIVEAVALDRMMEDGLQPTQITYGTIVDGMCKKGDTVSA	236
Query	239	LNLRRMEEVSHIIPNVVIYSAIIDSCLKDGRHSDAQNLFTEMOEKGIFPDLFYTNSMIV	298
Sbjct	237	LNLRRMEE-SHI PNVVIYSAIIDSCLKDGRHSDAQNLFTEMOEKGIFPDLFYTNSMIV	296
Query	299	GFCSSGRWSDAEQLQEMLERKISPDVVTYNALINAFVKEGKFEEAEELYDEMLPREGIIP	358
Sbjct	297	GFC SGRWS A+-LLQEMLERKISPDVVTYNALINAFVKEGKFEEAELYDEMLPREGIIP	356
Query	359	NTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPSPNLITFNTLIDGYCGAKRIDDGMELL	418
Sbjct	357	NTITY+SMIDGFCKQ+RLDAAE MFYLMATKGCPSP++ TF TLIDGYCGAKRIDDGMELL	416
Query	419	HEMTETGLVADTTTYNTLIGHFYLGVGDLNAA LDLLQEMISSGCPDIVTCDELLGLCDN	478
Sbjct	417	HEM GLVA-T TYNTLIGHF LVGDLNAA LDLLQEMISSGCPDIVTCDELLGLCDN	476
Query	479	GKLKDALEMFKVMQSKSKLDASHPFNGVEPDVQTYNLLISGLINEGKFLEAEELYEEMP	538
Sbjct	477	GKLKDALEMFK MOKSK DLDASHPFNGVEPDVQTYNLLISGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRDLDEATQMFDSMGSKSFSPNVVTFTTLINGYCKAGRVD	598
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRDLDEATQMF SMGSKSFSPNVVTFTTLINGYCKAGRVD	596
Query	599	DGLELFCEMGRRGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVPDTITIRNML	658
Sbjct	597	DGLELFCEMGRRGIVADAIIYITLICGFRKVGNINGALDIFQEMISSGVPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLELKQMSM	681
Sbjct	657	TG WSKEEL+RAVAMLE LQMS+	679

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against SEQ 5 from Brown provisional No. 2 (60/305,363)**

Score = 1368 bits (3541), Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
Sbjct	84	MLARCGFKCSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143

Group 5

Query	61	EDAIIDLFSMDLRSRPLPSVVFDFCKLGMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIIDLFSMDLRSRPLPSVVFDFCKLGMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPFALSTFGKITKLGHLHPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCSKLPFALSTFGKITKLGHLHPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSALN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSALN	323
Query	241	LLRKMEEVSHIIIPNVVIYSAIIDSLCKDRHSDAQNLTTEMQEKGIFPPDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIIPNVVIYSAIIDSLCKDRHSDAQNLTTEMQEKGIFPPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISPDVVTTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLQEMLERKISPDVVTTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPSPNLITFTNLIDGYCGAKRIDDGMELLHE	420
Sbjct	444	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPSPNLITFTNLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTYNTLIHGFLVGDLNALADDLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTYNTLIHGFLVGDLNALADDLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSRDLDEATQMFDMSGSKSFSPPNVTFTTLINGYCKAGRVDGG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSRDLDEATQMFDMSGSKSFSPPNVTFTTLINGYCKAGRVDGG	683
Query	601	LELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against SEQ 6 from Brown provisional No. 2 (60/305,363)

Score = 974 bits (2517), Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Group 5

Query 1	MLARVCGFKCSSSPAESAARLFCTR SIRDTLAKASGESCEAGFGGESLKQSGFHEIKGL	60
Sbjct 1	MLARV SSSPA SAARLFCTR SIR LAK S + E+GFGGESLKL+SGFHEIKGL	59
Query 61	EDAIDLFSMDLRSRPLPSVVDCKLMGVVVRMERPDLVISLYQKMERKQIRC DIYSFNIL	120
Sbjct 60	EDAIDL DM+RSPRLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	119
Query 121	IKCFCSCSKLPFALSTFGKITKLGHLPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct 120	+KCFCSCSKLPFALSTFGKITKL FH MKCFCSCSKLPFALSTFGKITKLG-----FH-----	145
Query 181	RPNVVTFTTLMNGLCREGRIVEAVALLDRM MEDGLQPTQITYGTIVDGMCKKGDTV SALN	240
Sbjct 146	P VVTF+TL+-+GLC E RI EA+ L +M + P +T+ T++G+C++G V A+ -PTVVFSTLLHGLCVEDR ISEADLFLHQMKC ---PNVVTFTTLMNGLCREGRVVEAVA	200
Query 241	LLRKMEEVSHIIIPNVYI SAIIDS LCKDGRHS DAQNLT FEMEQKG-IFPDLFTY----N	294
Sbjct 201	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ + LLDRMLE-DGLQPQN QITYGTIVDGMCKMGDTV SALNLLRKMEEVSHIKPNVVIWPLER RT	259
Query 295	SMIVGFCS SGRWS DAEQLLQEMLERK-ISP DVVTYNA LINAFVKEGKFEEAEELYDEMLP	353
Sbjct 260	MI GPCSS GRWS+A+QLLQEMLERK ISP DVVTYNA LINAFVKEGKFEEAEELYDEMLP CMINGFCSS GRW SE A QQLLQEMLERK KIS PDVVTYNA LINAFVKEGKFEEAEELYDEMLP	319
Query 354	RGI IPNTITYSSMIDGFC KQN RLDAEHMFYLMATKG CSPN LITF NTL IDGY CGA KRID	413
Sbjct 320	RG I PNTITYSSMIDGFC KQN RLDAEHMFYLMATKG CSPD II FTNL IAGY CRA KRVD	379
Query 414	GM LKHEMTE TGLV ADTTYNTL IHGF YLV GDLN A ALD LQEMISS GLCPD IV CDT LLD	473
Sbjct 380	G++LLHEMTE GLV+A+T TL IHGF VGD LNAA DLLQEM+SSG+CP++VTC+TLLD GIKL LHEMTE AGL VANTITY TT L IHGF CQVG DLNA A QD L LQEM VSSG VC PNV VT CNT LLD	439
Query 474	GLCDNGKLKALEMFKV M QKS KKD LDASHPF NGV EPDV QTY N I L ISGLINEGKFLEAEEL	533
Sbjct 440	GLCDNGKLKALEMFK M QKS K D+DASHPF NGV EPDV QTY N I L ISGLINEGKFLEAEEL GLCDNGKLKALEMFKAM QKS KMD IDASHPF NGV EPDV QTY N I L ISGLINEGKFLEAEEL	499
Query 534	YEEMPHRG I VPDT ITYSSMIDGLCKQS RL DEAT QMFD SMSG SKSF SPN VFTT LINGY CK	593
Sbjct 500	YEEMPHRG I VPDT ITYSSMIDGLCKQS RL DEAT QMFD SMSG SKSF SPN VFTT LINGY CK YEEMPHRG I VPDT ITYSSMIDGLCKQS RL DEAT QMFD SMSG SKSF SPN VFTT LINGY CK	559
Query 594	AGR VDDG LELF CEM GRRG I VANA ITY ITLIC GFRK VGN INGALD IFQEM I SS G VY P DT IT	653
Sbjct 560	AGR VDDG LELF CEM GRRG I VANA ITY ITL GFRK VGN INGALD IFQEM++ SGV Y P DT IT AGR VDDG LELF CEM GRRG I VANA ITY ITL IHGF RKR VGN INGALD IFQEM MAS G VY P DT IT	619
Query 654	IRNMLT G LWSKEELKRAVAM LEK LQMS M	681
Sbjct 620	IRNMLT G LWSKEELKRAVAM LEK LQMS M IRNMLT G LWSKEELKRAVAM LEK LQMS M	647

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 1 from Brown provisional No. 3 (60/308,736)

Group 5

Score = 521 bits (1341), Expect = 2e-145
 Identities = 261/395 (66%), Positives = 311/395 (78%), Gaps = 1/395 (0%)

Query 288	PDLFETYNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEEL	347
	P++ T+ +++ G C GR +A LL M+E + P+ +TY +++ K G A L	
Sbjct 4	PNVTTFTTLMNGLCREGRVVEAVALLDRMVEDGLQPQNQITYGTIVDGMCKMGDTVSALNL	63
Query 348	YDEMLPRGII-PNTITYSSMIDGFCKQNRLDAAEHMFYLMATKGCSNPNLITFNTLIDGYC	406
	+M I P+ + YS++IDG K R A++F M KG P++T++ +I+G+C	
Sbjct 64	LRKMEELSHIKPDVVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPPDIVTYSCMINGFC	123
Query 407	GAKRIDDGSELLHEMTETGLVADTTYTNTLIHGFYLVGDLNAADDLQEMISSGLCPDIV	466
	++ + LL EM + D T++ LI+ GDLN+ DLLQEMISSG+CP++V	
Sbjct 124	SSGKWSAQRLLQEMLVRKISPDPVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPNVV	183
Query 467	TCDTLLDGLCDNGKLKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISLINEGK	526
	TC+TLLDGLCD GKLDALEMFK MQKS D+DA+H FNGVEPDVQTYNILISLINEGK	
Sbjct 184	TCNTLLDGLCDRGLKDALEMFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISLINEGK	243
Query 527	FLEAAELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDMSGSKSFSPNVTFT	586
	FLEAAELYEEMPHRGIVPDT+TYSSMI+GLCKQSRLDEATQMFDMSGSKSFSPN+VTF T	
Sbjct 244	FLEAAELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDMSGSKSFSPNIVTFNT	303
Query 587	LINGYCKAGRVDGELFCEMGRRGIVANAITYITLICFRKVGNINGALDIFQEMISSG	646
	LI GYCKAG VDDGLELFCEMGRRGIVANAITYITLI GFRKVGNING+LDIFQEMISSG	
Sbjct 304	LITGYCKAGMVDDGLELFCEMGRRGIVANAITYITLIRGFRKVGNINGSLDIFQEMISSG	363
Query 647	VYPDTITIRNMLTGLWSKEELKRAVAMLEKQMSM	681
	VYPDTITIRNMLTGLWSKEELKRA+AMLE+LQMSM	
Sbjct 364	VYPDTITIRNMLTGLWSKEELKRALAMLEELQMSM	398

Score = 394 bits (1012), Expect = 2e-107
 Identities = 208/404 (51%), Positives = 265/404 (65%), Gaps = 22/404 (5%)

Query 180	CRPNVVFTTLMNGLCREGRIVEAVALLDRRMEDGLQPTQITYGTIVDGMCKKGDTVSAL	239
	C+PNVVFTTLMNGLCREGR+VEAVALLDRR+EDGLQP QITYGTIVDGMCK GDTVSAL	
Sbjct 2	CKPNVVFTTLMNGLCREGRIVEAVALLDRRMEDGLQPTQITYGTIVDGMCKKGDTVSAL	61
Query 240	NLLRKMEEVSHIIIPNNVIYSAIIDSLCKDGRHSDAQNLITEMQEKGIFPPDLFTYNSMIVG	299
	NLLRKMEEVSHI P+VVIYSAIID L KDGRH+DAQNLF EMQ+KGIFPD+ TY+ MI G	
Sbjct 62	NLLRKMEELSHIKPDVVVIYSAIIDGLWKDGRHTDAQNLFIEMQDKGIFPPDIVTYSCMING	121
Query 300	FCSSGRWSDAEQLLQEMLERKISPDVVTYNALINAFVKEGKFFEAEEELYDEMLPRGIIPN	359
	FCSSG+WS+A++LLQEML RKISPDPV++ LINA VKEG A++L EM+ G+ PN	
Sbjct 122	FCSSGRWSAQRLLQEMLVRKISPDPVVTFSGLINALVKEGDLNSAQDLLQEMISSGVCPN	181
Query 360	TITYSSMIDGFCKQNRLDAAEHMFYLM-----ATKGCPNLITFNTLIDGYCGA	408
	+T +++DG C + L A MF M A G P++ T+N LI G	
Sbjct 182	VVTCTNLLDGLCDRGLKDALEMFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISLINE	241

Group 5

Query	409	KRIDDGMELLHEMTEGVLVADTTTNTLIGHFYLVGDLNAALDLLQEMISSLCPDIVTC	468
	+	EL EM G+V DT TY++I+G L+ A + M S P+IVT	
Sbjct	242	GKFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMSGSKSFSPNIVTF	301
Query	469	DTLDGLCDNGKLKDALEMFKVMQSKKKLDASHPFNGVEPDVQTYNILISGLINEGKFL	528
	+TL+ G C G + D LE+F M +	G+ + TY LI G G	
Sbjct	302	NTLITGYCKAGMVDDGLELFCEMGR-----RGIVANAITYTLLIRGFRKVGNIN	350
Query	529	EAEELYEEMPHRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSM	572
	+ ++++EM G+ PDTIT +M+ GL + L A M + +		
Sbjct	351	GSLDIFQEMISSLGVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 300 bits (767), Expect = 6e-79
 Identities = 166/395 (42%), Positives = 229/395 (57%), Gaps = 48/395 (12%)

Query	147	PDVVFTTLLHGLCVERVSEALDFHFQMFFETTCRPNVVFTTLMNGLCREGRIVEAVAL	206
	P+VVTFTT+GLC E RV EA+ +M E -PN +T+ T++G+C G V A+ L		
Sbjct	4	PNVVFTTLLMNGLCREGRVVEAVALDRMVEDGLQPQNITYGTIVDGMCMDTWSALNL	63
Query	207	LDRMME-DGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIIPNPNVISSAIIDLS	265
	L +M E ++P + Y I=DG+ K G A NL +M++ I P+v YS +I+		
Sbjct	64	LRKMEELSHIKPDDVVIYSIAIIDGLWKDRHTDAQNLFIEMQD-KGIFPDIVTYSCMINGF	122
Query	266	CKDGRHSDAQNLFTEMQEKGIFPDLFETYNSMIVGFCSSGRWSDAEQLLQEMLE-----	318
	C G+ S=AQ L EM + I PD+ T++ +I G + A+ LLQEM+		
Sbjct	123	CSSGKWESEAQRLLQEMLVRKISPDVVTFSGLINALVKEDDLNSAQDLLQEMISSLGVCPNV	182
Query	319	-----RKISPDVVTYNALINAFVKEG	339
	+ PDV TYN LI+ + EG		
Sbjct	183	VTCNTLTDGLCDRGKLKDALEMFKAMQSMSMDIDATHAFNGVEPDVQTYNILISGLINEG	242
Query	340	KFFEAEEELYDEMLPRGIIPNNTITYSSMIDGFCKQNRLDAEAEHMFYLMATKGCSNPNLITFN	399
	KF EAEELY-EM RGI+P+T+TYSSMI+G CKQ+RLD A MF M + K SPN++TFN		
Sbjct	243	KFLEAEELYEEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMSGSKSFSPNIVTFN	302
Query	400	TLIDGYCKAKRIDDGMELLHEMTEGVLVADTTTNTLIGHFYLVGDLNAALDLLQEMISSL	459
	TLI GYC A +DDG+EL EM G+VA+ TY TLI GF VG++N +LD+ QEMISS		
Sbjct	303	TLITGYCKAGMVDDGLELFCEMGRGIVANAITYTLLIRGFRKVGNINGSLDIFQEMISS	362
Query	460	GLCPDIVTCDTLLDGLCDNGKLKDALEMFKVMQKS	494
	G+ PD +T +L GL +LK AL M + +Q S		
Sbjct	363	GVYPDTITIRNMLTGLWSKEELKRALAMLEELQMS	397

Score = 216 bits (551), Expect = 7e-54
 Identities = 120/392 (30%), Positives = 214/392 (54%), Gaps = 13/392 (3%)

Group 5

Query	77	PSVVDCKLGMVVVRMERRPDLVISLYQKMERKQIRCDIYSFNILIKCFCSCSKLPFALST	136
Sbjct	4	PNNVTTTLMNGLCREGRVVEAVALLDLRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNL	63
Query	137	FGKITKLG-LHPDVVTFTTLLHGLCVERVSEALDFHHQMFFETTCRPNVFTTLMNGLC	195
Sbjct	64	K+ -L + PDVV ++ ++ GL + R ++A + F +M + P++VT++ ++NG C	123
Query	196	REGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALNLLRKMEEVSHIIPNV	255
Sbjct	124	G+ EA LL M+ + P +T+ +++ + K+GD SA +LL+ +M S + PNV SSGKWSAQRLQEMLVRKISPDVVTFTSGLINALVKEGDLNSAQDLQEMIS-SGVCPNV	182
Query	256	VIYSAIDISSLCKDGRHSADQNLTEMQE-----KGIFPDLFYTNSMIVGFCSSG	304
Sbjct	183	V+ ++D LC G+ DA +F MQ+ G+ PD+ TYN +I G + G VTCNTL LDGLCDRGKLDKALEMFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISGLINEG	242
Query	305	RNSDAEQLLQEMLERKISPDVVTYNAFLVKEGKFEEAEELYDEMLPREGIIPNITYS	364
Sbjct	243	++ +AE+L +EM R I PD VTY+ ++IN K+ + EA + ++D M + PN +T++ KFLEAAELYEEMPHRGIVPDVTYSSMINGLCKQSRLDEATQMFDSMSGSKSFSPNIVTFN	302
Query	365	SMIDGFCKQNRLDAAEHMFYLMATKGCSPLNLTIFNTLIDGYCGAKRIDGMELLHEMTET	424
Sbjct	303	++I G+CK +D +F M +G N IT+ TLI G+ I+ + ++ EM + TLITGYCKAGMVDDGLELFCEMGRGGIVANAIYTITLIRGFRKVGNINGSLIDFQEMISS	362
Query	425	GLVADTTTYNTLIGHFYLVGDLNAALDLLQEM	456
Sbjct	363	G+ DT T ++ G + +L AL +L+E+ GVYPDTITIRNMLTGLWSKEELKRALAMLEEL	394

Score = 193 bits (491), Expect = 6e-47
 Identities = 109/371 (29%), Positives = 193/371 (52%), Gaps = 11/371 (2%)

Query	62	DAIDLSDMLRSRPLPSVVDCKLGMVVVRMERRPDLVISLYQKMER-KQIRCDIYSFNIL	120
Sbjct	24	+A+ L M+ P+ + + +M ++L +KME I+ D+ ++ + EAVALLDLRMVEDGLQPNQITYGTIVDGMCKMGDTVSALNLLRKMEELSHIKPDVVIYSAI	83
Query	121	IKCFCSCSKLPFALSTFGKITKLGHDLPDVFTTLLHGLCVERVSEALDFHHQMFFETTC	180
Sbjct	84	I+ A + F ++ G+ PD+VT++ +++G C + SEA +M IDGLWKDGRHTDAQNLFIEMQDKGIFPDIVTYSMINGFCSSGKWSAQRLQEMLVRKI	143
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKKGDTVSALN	240
Sbjct	144	P+VVT+ L+N L +EG + A LL M+ G+ P +T T++DG+C +G AL SPDVTFSGLINALVKEGDLNSAQDLQEMISSGVCNVTCNTL LDGLCDRGKLDALE	203
Query	241	LLRKME-----EVSH----IIIPNVVIYSAIDISSLCKDGRHSADQNLTEMQEKGIFPD	290
Sbjct	204	+ +M+ + +H + P+V Y+ +I L +G+ +A+ L+ EM +GI PD MFKAMQKSMMIDIDATHAFNGVEPDVQTYNILISGLINEGKFLEAAELYEEMPHRGIVPDT	263
Query	291	FTYNNSMIVGFCSSGRWSDAEQLLQEMLERKISPDVVTYNAFLVKEGKFEEAEELYDE	350
Sbjct	264	TY+SMI G C R +A Q+ M + SP++VT+N LI + K G + EL+ E VTYSSMINGLCKQSRLDEATQMFDSMSGSKSFSPNIVTFNTLITGYCKAGMVDDGLELFCE	323

Group 5

Query 351	MLPRGIIIPNNTITYSSSMIDGFCKQNRLLDAAEHMFYLMATKGCSPLNLITFNTLIDGYCGAKR	410
M RGI+ N ITY ++I GF K + + + +F M + G P+ IT ++ G +		
Sbjct 324	MGRRGIVANAITYITLIRGFRKVGNNINGSLDIFQEMISSGGVYPDTITIRNMLTGLWSKEE	383
Query 411	IDDGMELLHEM 421	
+ + +L E+		
Sbjct 384	LKRALAMLEEL 394	

Score = 118 bits (296), Expect = 3e-24
 Identities = 78/282 (27%), Positives = 130/282 (46%), Gaps = 12/282 (4%)

Query 52	SGFHEIKGLEDAIDLFSMLRSRPLPSVVDFCKLGVVRMERPDLVISLYQKMERKQIR	111
+GF	+A L +ML + P VV F L+ +V+ + L Q+M +	
Sbjct 120	NGFCSSGKWSEAQRLQEMVLVRKISPDVFTFSGLINALVKEGDLNSAQDLLQEMISSGVC	179
Query 112	CDIYSFNILIKCFCSCSKLPFALSTFGKITKL-----GLHPDVVTFTTLHGLC	160
++ + N L+ C KL AL F + K	G+ PDV T+ L+ GL	
Sbjct 180	PNVVTCTNLLDGLCDRGKLKDALEMFKAMQKSMMIDATHAFNGVEPDVQTYNILISGLI	239
Query 161	VEDRVSEALDFFHQMFFETTCRPNVVTFTLMNGLCREGRIVEAVALLDRMMEDGLQPTQI	220
E + EA + + +M	P+ VT+++++NGLC++ R+ EA + D M P +	
Sbjct 240	NEGKFLEAEELYEMPHRGIVPDTVTYSSMINGLCKQSRLDEATQMFDSMGSKSFPNIV	299
Query 221	TYGTIVDGMCKKGDTVSALNLLRKMEEVSHPNVVIYSAIIDSCLKDGRHSDAQNLFT	280
T+ T++ G CK G L L -M	I+ N + Y +I K G + + ++F E	
Sbjct 300	TFNTLITGYCKAGMVDDGLELFCEMRRG-IVANAITYITLIRGFRKVGNNINGSLDIFQE	358
Query 281	MQEKGIFPPDLFTYNSMIVGFCSSGRWSDAEQLQEMLERKIS	322
M G++PD T +M+ G S A +L+E+ +S		
Sbjct 359	MISSGVYPDTITIRNMLTGLWSKEELKRALAMLEELQMSMVS	400

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 2 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 3 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 4 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 5 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found

Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 6 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 7 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 8 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 9 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 10 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 11 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 12 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 13 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 14 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 15 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 16 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found

Group 5

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 17 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 18 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 19 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 20 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 21 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 22 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 23 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 24 from Brown provisional No. 3 (60/308,736)**

Score = 1179 bits (3049), Expect = 0.0
Identities = 594/683 (86%), Positives = 628/683 (91%), Gaps = 6/683 (0%)

Query 1	MLARVCGFKCSSSPAESAARLFCTRSLAKAS--GESCEAGFGGESLKLQSGFHEIK	58
	MLARVC F+ SSS + SAAR FCT SIR LA+ S GES EAGF GESLKL+SG +EIK	
Sbjct 1	MLARVCRFESSSSSSVAARFFCTGSIRHALAEKSRSRGEAGFRGESLKLRSGSYEIK	60
Query 59	GLEDAIDLFSMDLRLSRPLPSVVDFCKLGMVVVRMERPDVLVISLYQKMERKQIRCDIYSFN	118
	GLEDAIDLFSMDLRLSRPLPSV+DF KLMG VVRMERPDVLVISLYQKMERKQIRCDIYSF	
Sbjct 61	GLEDAIDLFSMDLRLSRPLPSVIDFNKLGMGVVRMERPDVLVISLYQKMERKQIRCDIYSFT	120
Query 119	ILIKCFCSCKLPFALSTFGKITKGLLHPDVVTFTTLLHGLCVEDRVSSEALDFFHQMFT	178
	ILIKCFCSCKLPFALSTFGK+TKLGLLHPDVVTFTTLLHGLC++ RVSEALD FHQ+	
Sbjct 121	ILIKCFCSCKLPFALSTFGKLTKLGLLHPDVVTFTTLLHGLCLDHRVSEALDFHQI---	177

Group 5

Query	179	TCRPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSA	238
		CRP+V-TFTTLMNGLCREGR+VEAVALLDRM+E+GLQP QITYGT VDGMCK GDTVSA	
Sbjct	178	-CRPDVLTTFTTLMNGLCREGRVVEAVALLDRMVENGLOPDQITYGTIVDGMCKGDTVSA	236
Query	239	LNLLRKMEEVSHIIPNVVIYSAIIDSLCKDGRHSDAQNLFTEMQEKGIFPDLFYTNSMIV	298
		LNLLRKME-E-SHI PNVVIYSAIID LCKDGRHS+ NLF EMQ+KGIFP++ TYN MI	
Sbjct	237	LNLLRKMEEISHIKPNVVIYSAIDGLCKDGRHSASHNLFIEMQDKGIFFPNIVTYNCMIG	296
Query	299	GFCSSGRWSDAEQLLQEMLERKISPDVVNTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	358
		GFC SGRWS A+-LLQEMLERKISP+VVVNTYNALINAFVKEGKFFEA ELYDEMLPRGIIP	
Sbjct	297	GFCISGRWSAAQRLLQEMLERKISPNVVTYNTYNALINAFVKEGKFFEAEEELYDEMLPRGIIP	356
Query	359	NTITYSSMIDGFCKQNRLDAAEHHMFYLMATKGCSPLNTLIDGYCGAKRIDDGMELL	418
		NTITY-SMIDGFCKQ-RLDAAE MFYLMATKGCSPP+ TF TLIDGYCGAKRIDDGMELL	
Sbjct	357	NTITYNSMIDGFCKQDLDAADMFYLMATKGCSPLVFTTLIDGYCGAKRIDDGMELL	416
Query	419	HEMTGLVADTTTYNTLIGHFVLGDLNAADDLQLQEMISSGLCPDIVTCDTLLDGLCDN	478
		HEM GLVA+T TYNTLIGHF LVGDLNAALLD Q+MISSG+CPDIVTC+TLLDGLCDN	
Sbjct	417	HEMPRRGLVANTVNTLIGHFCLVGDLNAALDLQQMISSGVCPDIVTCNTLLDGLCDN	476
Query	479	GKLKDALEMFKVMQSKKDDLDASHPFNGVEPDVQTYNILISGLINEGKFLEAEELYEEMP	538
		GKLKDALEMFK MQSK DLDASHPFNGVEPDV TYNILI GLINEGKFLEAEELYEEMP	
Sbjct	477	GKLKDALEMFKAMQSKKMDLDASHPFNGVEPDVLTNYNILICGLINEGKFLEAEELYEEMP	536
Query	539	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFDSMGSKSFSPNVFTTLINGYCKAGRVD	598
		HRGIVPDTITYSSMIDGLCKQSRLDEATQMF SMGSKSFSFSPNVFTT TLINGYCKAGRVD	
Sbjct	537	HRGIVPDTITYSSMIDGLCKQSRLDEATQMFVSMGSKSFSFSPNVFTNTLINGYCKAGRVD	596
Query	599	DGLELFCEMGRRGIVANAITYITLICGKVGNINGALDIFQEMISSGGVPDTITIRNML	658
		DGLELFCEMGRRGIVVA-AI YITL GFRKVGNINGALDIFQEMISSGGVPDTITIRNML	
Sbjct	597	DGLELFCEMGRRGIVADAIYIYTLYGFRKVGNINGALDIFQEMISSGGVPDTITIRNML	656
Query	659	TGLWSKEELKRAVAMLEKLQMSM 681	
		TG WSKHEEL-RAVAMLE LQMS+	
Sbjct	657	TGFWSKHEELERAVAMLELDLQMSV 679	

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 25 from Brown provisional No. 3 (60/308,736)**
 - No significant similarity was found
- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 26 from Brown provisional No. 3 (60/308,736)**

Score = 1368 bits (3541), Expect = 0.0
 Identities = 681/681 (100%), Positives = 681/681 (100%), Gaps = 0/681 (0%)

Query	1	MLARVCGFCKSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	60
		MLARVCGFCKSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	
Sbjct	84	MLARVCGFCKSSSPAESAARLFCTRSIRDTLAKASGESCEAGFGGESLKLQSGFHEIKGL	143

Group 5

Query	61	EDAIIDLFSMDLRSRPLPSVVFDFCKLGMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNIL	120
Sbjct	144	EDAIIDLFSMDLRSRPLPSVVFDFCKLGMGVVVRMERPDVLVISLYQKMERKQIRCDIYSFNIL	203
Query	121	IKCFCSCSKLPFALSTFGKITKLGHLHPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct	204	IKCFCSCSKLPFALSTFGKITKLGHLHPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	263
Query	181	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSALN	240
Sbjct	264	RPNVVTFTTLMNGLCREGRIVEAVALLDRMMEDGLQPTQITYGTIVDGMCKGDTVSALN	323
Query	241	LLRKMEEVSHIIIPNVVIYSAIIDSLCKDRHSDAQNLTTEMQEKGIFPPDLFTYNSMIVGF	300
Sbjct	324	LLRKMEEVSHIIIPNVVIYSAIIDSLCKDRHSDAQNLTTEMQEKGIFPPDLFTYNSMIVGF	383
Query	301	CSSGRWSDAEQLLQEMLERKISPDVVTTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	360
Sbjct	384	CSSGRWSDAEQLLQEMLERKISPDVVTTYNALINAFVKEGKFFAEELYDEMLPRGIIPNT	443
Query	361	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPSPNLITFTNLIDGYCGAKRIDDGMELLHE	420
Sbjct	444	ITYSSMIDGFCKQNRLDAAEHMFYLMATKGCPSPNLITFTNLIDGYCGAKRIDDGMELLHE	503
Query	421	MTETGLVADTTTYNTLIHGFLVGDLNALADDLQEMISSGLCPDIVTCDTLLDGLCDNGK	480
Sbjct	504	MTETGLVADTTTYNTLIHGFLVGDLNALADDLQEMISSGLCPDIVTCDTLLDGLCDNGK	563
Query	481	LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISLINEGKFLEAEELYEEMPHR	540
Sbjct	564	LKDALEMFKVMQSKKDLDASHPFNGVEPDVQTYNILISLINEGKFLEAEELYEEMPHR	623
Query	541	GIVPDTITYSSMIDGLCKQSRDLDEATQMFDMSGSKSFSNPVVTFTTLINGYCKAGRVDGG	600
Sbjct	624	GIVPDTITYSSMIDGLCKQSRDLDEATQMFDMSGSKSFSNPVVTFTTLINGYCKAGRVDGG	683
Query	601	LELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	660
Sbjct	684	LELFCEMGRGGIVANAITYITLICGFRKVGNINGALDIFQEMISSGVYPDTITIRNMLTG	743
Query	661	LWSKEELKRAVAMLEKLQMSM	681
Sbjct	744	LWSKEELKRAVAMLEKLQMSM	764

- **SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 27 from Brown provisional No. 3 (60/308,736)**

Score = 974 bits (2517), Expect = 0.0
 Identities = 510/688 (74%), Positives = 568/688 (82%), Gaps = 48/688 (6%)

Group 5

Query 1	MLARVCGFKCSSSPAESAARLFCTR SIRDTLAKASGESCEAGFGGESLKQSGFHEIKGL	60
Sbjct 1	MLARV SSSPA SAARLFCTR SIR LAK S + E+GFGGESLKL+SGFHEIKGL	59
Query 61	EDAIIDLFSDMRLSRPPLPSVVDCKLMGVVVRMERPDLVISLYQKMERKQIRC DIYSFNIL	120
Sbjct 60	EDAIIDL DM+RSPRPLPSV+DFCKLMGVVVRM R D+VISL++KME +++ C+ YSF IL	119
Query 121	IKCFCSCSKLPFALSTFGKITKLGHLPDVVTFTLLHGLCVEDRVSEALDFFHQMFETTC	180
Sbjct 120	+KCFCSCSKLPFALSTFGKITKL FH MKCFCSCSKLPFALSTFGKITKLG-----FH-----	145
Query 181	RPNVVTFTTLMNGLCREGRIVEAVALLDRM MEDGLQPTQITYGTIVDGMCKKGDTV SALN	240
Sbjct 146	P P VTF+TL+-+GLC E RI EA+ L +M + P +T+ T++G+C++G V A+ -PTVVFSTLLHGLCVEDR ISEALDLFHQMCK---PNVVTFTTLMNGLCREGRVVEAVA	200
Query 241	LLRKMEEVSHIIIPNVYSAIIDS LCKDGRHS DAQNLT FEMEQKG-IFPDLF TY----N	294
Sbjct 201	LL +M E + PN + Y I+D +CK G A NL +M+E I P++ + LLDRMLE-DGLQPQN QITYGTIVDGMCKMGDTV SALNLLRKMEEVSHIKPNVVIWPLER RT	259
Query 295	SMIVGFCSGRWSDAEQLLQEMLERK-ISP DVVTYNA LINAFVKEGKFEEAEELYDEMLP	353
Sbjct 260	MI GPCSSGRWS+A+QLLQEMLERK ISP DVVTYNA LINAFVKEGKFEEAEELYDEMLP CMINGFCSSGRWSEAQQLLQEMLERK KISP DVVTYNA LINAFVKEGKFEEAEELYDEMLP	319
Query 354	RGIIPNTITYSSMIDGFC KQNRLDAAEHM FYLMA TKG CSPN LITF NTL IDGY CGA RIDD	413
Sbjct 320	RGIIPSTITYSSMIDGFC KQNRLDAAEHM FYLMA TKG CSPD II T FNTL IAGY CRA KRVD	379
Query 414	GMNLHEMTE TGLVADTTYNTL IHGFYLVGD LNAA LDQEMISS GLCPD IVTCD TLLD	473
Sbjct 380	G++LLHEMTE GLV+T TY IHGF VGDL NAA DLLQEM+SSG+CP++VTC+TLLD GI KLHEMTE AGLVANTITYTTL IHGF CQVG DLNAA QD LQEM VSSG VCPN VTCNTLL	439
Query 474	GLCDNGKLKDALEMF KV M QKSKKD L DASHPF NGV EPDV QTYN ILISGLINEGKFLEAEEL	533
Sbjct 440	GLCDNGKLKDALEMF K MQKSK D+DASHPF NGV EPDV QTYN ILISGLINEGKFLEAEEL GLCDNGKLKDALEMF K AMQKSKMDIDASHPF NGV EPDV QTYN ILISGLINEGKFLEAEEL	499
Query 534	YEEMPHRGIV P D TITYSSMIDGLCKQS RLDEATQ MFDS MGSKSF SPN VFT TLINGYCK	593
Sbjct 500	YEEMPHRGIV P D TITYSSMIDGLCKQS RLDEATQ MFDS MGSKSF SPN VFT TLINGYCK YEEMPHRGIV P D TITYNSVIHGLCKQS RLDEATQ MFDS MGSKSF SPN VFT TLINGYCK	559
Query 594	AGR VDDGLELFCEM GRRGIVANA ITLICGFRKVGN INGALDIFQEMI SS GVYPDTIT	653
Sbjct 560	AGR VDDGLELFCEM GRRGIVANA ITLICGFRKVGN INGALDIFQEM+ +SGVYPDTIT AGR VDDGLELFCEM GRRGIVANA ITLICGFRKVGN INGALDIFQEMMASGVYPDTIT	619
Query 654	IRNMLTGLWSKEELKRAVAM LEKLQMSM 681	
Sbjct 620	IRNMLTGLWSKEELKRAVAM LEKLQMSV 647	

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 28 from Brown provisional No. 3 (60/308,736)

Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 29 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 30 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 31 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 32 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 33 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 34 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 35 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 36 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 37 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 38 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 39 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found

Group 5

- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 40 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 41 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 42 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found
- SEQ 3 from Japanese application from January 2002 (JP 2002-020083)against PRT SEQ 43 from Brown provisional No. 3 (60/308,736)
 - No significant similarity was found